

Thu Apr 11 12:31:15 2002

us-09-609-543-2.rai

Page 8

[illegible]

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REGENT 15
DS 09 103 079 17
SEQUENCE 17, Application US/09103079A
Patent No. 6013477
GENERAL INFORMATION:
APPLICANT: Greenberg, John M.
APPLICANT: Resner, Craig A.
TITLE OF INVENTION: Filtrolast Growth Factor 15
FILE REFERENCE: P20301
CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION NUMBER: 08/466,216
EARLIER FILING DATE: 1995-06-05
NUMBER OF STEPS TO PUS: 3,2
SOFTWARE: Patent In Vot. 2.0
SEQ ID NO: 17
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
DS 09 103 079 17

```

[illegible]

```

1 ADDRESS: ADDRESS:
2 ADDRESSEE: Fish & Richardson P.C.
3 STREET: 4225 Executive Square, Suite 1400
4 CITY: La Jolla
5 STATE: CA
6 COUNTRY: USA
7 ZIP: 92037
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM pc compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: Patent Release #1.0, Version #1.30
13 CURRENT APPLICATION DATA:
14 ATTORNEY/CLIENT REFERENCE: 05/29/705, 245
15 FILING DATE: 30-AUG-1996
16 CLASSIFICATION: 530
17 ATTORNEY/CLIENT INFORMATION:
18 NAME: Wetzel, J. & John R.
19 REGISTRATION NUMBER: 31,676
20 REFERENCE: 44,499-46,499-094001
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: 619/678-5070
23 TELEFAX: 619/678-50999
24 INFORMATION FOR SEQ ID NO: 7:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 208 amino acids
27 TYPE: amino acid
28 STRANDINGS: not relevant
29 TOPOLOGY: linear
30 MOLECULE TYPE: protein
31
32 US-08 705-245-7

```

[illegible]

APPLICANT: SEKI, Sachiko

GENERAL INFORMATION:
APPLICANT: NAKIDO, Ken-ichi

1. *What is the purpose of this study?*


```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/340,820
3 FILING DATE:
4 CLASSIFICATION: 435
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 09/07,835,713
7 FILING DATE:
8 ATTORNEY/AGENT INFORMATION:
9 NAME: GOSLIP, David G.
10 REGISTRATION NUMBER: 27026
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: (417)523-3400
13 TELEFAX: (417)524-6440
14 TELEX: 200291 STPE OR
15 INFORMATION FOR SEQ. ID NO. 5:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 205 amino acids
18 TYPE: amino acid
19 TOPOLOGY: linear
20 MOLECULE TYPE: protein
21 US 08-340-820-5

```

Query Match	67.8%	Score 758.5	DB 1	Length 2052	
Host Local Similarity	70.28%	Prod. No. 1-20	772		
Matches 1462	Conserved 156	23%	Matches 402	Indels 9	Gaps
Q7	4	LAEEVAPLEGLRLGAGVSWSHFLDPPAFGEKRLIADERSAAERSAAGC--GPGAAQLAIL	60		
		1 1			
Db	1	LAEEVAPVYVQVAV--PPEVNVVLYV--DSPVLSIDHLDGSE--AGGLDGGVAVTIDH	64		
Q7	61	HEILKEKQLYCKTGTGPHGLDLPESVSGCTAQHDSITELLLEFISAVAVLSTKPVLSCTLYG	120		
		1 1			
Db	55	KILLERKQLYCKTGTGPHGLDLPENGLTGGIKRHSRDLLEFISAVAVLSTKPVLSCTLYG	114		
Q7	121	RMKRLKLYSSEKLSLSELEFEEELTLMKRYSTSGNLRKELDPEPVVALSKPGLPEKQAK	180		
		1 1			
Db	115	RMKRLKLYSSEKLSLSEVTRKQFLDMKRYSTSGNLRKELDPEPVVALSKPGLPEKQAK	174		
Q7	141	SKRHQKFLHFLDPPVDPPEVPELYKILL	208		
		1 1			
Db	175	SKRHQKFLHFLDPPVDPPEVPELYKILL	202		

RESULT 25
 DB: 08-17-2-328-4
 7 September 4, Affiliation: 05709172328

1 RESULT: 25
 2 US:08-172-328-4
 3 Sequence #: 1
 4 Application US:08172328
 5 Patient No: 5571895
 6 GENERAL INFORMATION:
 7 APPLICANT: KUROKAWA, Tsutomu
 8 APPLICANT: KUROKAWA, Ken-ichi
 9 APPLICANT: YOSHITOMI, Sumie
 10 APPLICANT: SAKO, Sachiko
 11 TITLE OF INVENTION: ANTIBODIES, POLYPEPTIDES, PRODUCTION AND
 12 TITLE OF INVENTION: USE THEREOF
 13 NUMBER OF SEQUENCES: 12
 14 CORRESPONDENT ADDRESS:
 15 ADDRESSEE: DAVO G. COULIN, JR., BROOKFIELD, CONNECTICUT 06005 &
 16 ADDRESSEE: CUSHMAN
 17 STREET: 140 Water Street
 18 CITY: Boston
 19 STATE: Massachusetts
 20 COUNTRY: US
 21 ZIP: 02109
 22 COMPUTER READABLE FORM:
 23 MEDIUM TYPE: Floppy disk
 24 COMPUTER: IBM pc compatible
 25 OPERATING SYSTEM: PC DOS/MS-DOS
 26 SOFTWARE: Patent In Release #1.0, Version #1.25
 27 CURRENT APPLICATION DATA:
 28 APPLICATION NUMBER: 55708172, 328
 29 FILING DATE:
 30 CLASSIFICATION: 445

ALTERNATIVE SOURCE: HEP. SMITHSONIAN
 NAME: NEUDER, George W
 REGISTRATION NUMBER: 26964
 REFERENCE/ELECTRONIC NUMBER: 26964
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)523-4400
 TELEFAX: (617)523-6410
 TELEAX: 200291 519E 99
 INFORMATION IN THIS FILE IS NOT
 EQUIVOCAL CHARACTERISTICS:
 LENGTH: 205 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYDROPHILIC: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 HAPLOTYPE: 2n
 TISSUE TYPE: SKIN
 CELL TYPE: Fibroblast
 IMMEDIATE SOURCE:
 LIBRARY: Human foreskin cDNA library
 CLONED: pGAF1
 INS-08-172-328-4

APPLICATION NUMBER: US/07/2845 714
 FILING DATE:
 AUTONOMY/AGENT INFORMATION:
 NAME: COHLIN, David G.
 REGISTRATION NUMBER: 27026
 TELEPHONE: (617) 523-4400
 TELEFAX: (617) 523-6440
 TELE: 200291 STRE OR
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 206 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-340-820-7

Query Match 67.8% Score 758.51 DB 1: Length 206;
 Best Local Similarity 70.2% Pred. No. 1,2e-77;
 Matches 146; Conserved 23; Mismatches 30; Indels 9; Gaps 4;

QY 4 LAWVGGFAGLGLDGLDQVGSHPFLDPVGRPTLADKRSAAKRSARQ--GPGAAQALAH 60
 1
 DB 2 LGEVNYFVQVAV- PPGNVVLYV DSVLLSHLDQSE AGGAPRGAVVTHLDH 55
 1
 QY 61 HELLKRGQVYKGTGHLGLTPKRSVGTGKQHSIPGLLEPISAVAVLSTKQVSLYLQ 120
 1
 DB 56 KILLKRGQVYKGTGHLGLTPKRSVGTGKQHSIPGLLEPISAVAVLSTKQVSLYLQ 115
 1
 QY 121 MKRKGKYSKSLSSQSLFPGSLDWNH--LHLLTHDGLGKLYVA--REGCEPEGLAR 180
 1
 DB 116 MKRKGKYSKSLSSQSLFPGSLDWNH--LHLLTHDGLGKLYVA--REGCEPEGLAR 175
 1
 QY 181 SKRDKFTHTLPRVDPKRPVPELYKDL 208
 1
 DB 176 TKRDKFTHTLPRVDPKRPVPELYKDL 204
 1

RESULT 28
 US-08-340-820-8
 Sequence 8, Application US/08/40820
 Patient No. 5571895
 GENERAL INFORMATION:
 APPLICANT: NAKAG, Ken-ichi
 APPLICANT: SAKO, Chisako
 APPLICANT: KUROKAWA, Isotomo
 APPLICANT: KUROKAWA, Ken-ichi
 APPLICANT: KOSHIHIMA, Sumio
 TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DAVID G. COHLIN, DKE, ROSENSTEIN, ROBERTS &
 ADDRESS: CUSHMAN
 STREET: 140 WATER STREET
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: US
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: pc dos/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/40820
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/2845 714
 FILING DATE:
 AUTONOMY/AGENT INFORMATION:
 NAME: COHLIN, David G.

REGISTRATION NUMBER: 27026
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 523-4400
 TELEFAX: (617) 523-6440
 TELIX: 200291 STRE OR
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 206 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-340-820-8

Query Match 67.8% Score 758.51 DB 1: Length 206;
 Best Local Similarity 70.2% Pred. No. 1,2e-77;
 Matches 146; Conserved 23; Mismatches 30; Indels 9; Gaps 4;

QY 4 LAWVGGFAGLGLDGLDQVGSHPFLDPVGRPTLADKRSAAKRSARQ--GPGAAQALAH 60
 1
 DB 2 LGEVNYFVQVAV- PPGNVVLYV DSVLLSHLDQSE AGGAPRGAVVTHLDH 55
 1
 QY 61 HELLKRGQVYKGTGHLGLTPKRSVGTGKQHSIPGLLEPISAVAVLSTKQVSLYLQ 120
 1
 DB 56 KILLKRGQVYKGTGHLGLTPKRSVGTGKQHSIPGLLEPISAVAVLSTKQVSLYLQ 115
 1
 QY 121 MKRKGKYSKSLSSQSLFPGSLDWNH--LHLLTHDGLGKLYVA--REGCEPEGLAR 180
 1
 DB 116 MKRKGKYSKSLSSQSLFPGSLDWNH--LHLLTHDGLGKLYVA--REGCEPEGLAR 175
 1
 QY 181 SKRDKFTHTLPRVDPKRPVPELYKDL 208
 1
 DB 176 TKRDKFTHTLPRVDPKRPVPELYKDL 204
 1

RESULT 29
 US-08-172-328-5
 Sequence 5, Application US/08/172328
 Patient No. 5571895
 GENERAL INFORMATION:
 APPLICANT: KUROKAWA, Isotomo
 APPLICANT: KOSHIHIMA, Ken-ichi
 APPLICANT: YOSHITOMI, Sumio
 APPLICANT: SAKO, Chisako
 TITLE OF INVENTION: ANTIPODES, POLYPEPTIDES, PRODUCTION AND
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DAVID G. COHLIN, DKE, ROSENSTEIN, ROBERTS &
 ADDRESS: CUSHMAN
 STREET: 140 WATER STREET
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: US
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: pc dos/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/172 328
 FILING DATE:
 CLASSIFICATION: 435
 AUTONOMY/AGENT INFORMATION:
 NAME: NAKAG, Ken-ichi
 REGISTRATION NUMBER: 26964
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 523-4400
 TELEFAX: (617) 523-6440
 TELIX: 200291 STRE OR
 INFORMATION FOR SEQ ID NO: 5:

100

RESULT: 39
 US-08-172-328-19
 ; Sequence 9, Application US/08172328
 ; Patent No. 5571995
 ; GENERAL INFORMATION:

RESULT: 40
US-08-438-4397-21
Sequence 21, Application US/084384397
Patent No. 5876967
GENERAL INFORMATION:
APPLICANT: Mathias, Jeremy

APPLICATION NUMBER: 92759743.917
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MAZEA, Richard J.
 REGISTRATION NUMBER: 27,657
 REFERENCE/BOOKLET NUMBER: A-469
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 805.447.4112
 TELEFAX: 805.447.1090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 207 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 PS-OR-IG: 94.8-91.5-2


```

1 STREET: 140 Water Street
2 CITY: Boston
3 STATE: Massachusetts
4 COUNTRY: US
5 ZIP: 02109
6
7 COMPUTER AVAILABLE: YES
8 MEDIUM TYPE: floppy disk
9 COMPUTER: IBM pc compat 100
10 OPERATING SYSTEM: PC DOS/MS DOS
11 SOFTWARE: Patout In Release #1.0, Version #1.25
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/09/943 543
14 FILING DATE: 24 JAN 1996
15 CLASSIFICATION: 435
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 07/845,713
18 FILING DATE: 12 FEB 1992
19 AGENT/AGENT INFORMATION:
20 NAME: CONLIN, David G.
21 REGISTRATION NUMBER: 27026
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (617)524 4400
24 TELEFAX: (617)524 4440
25 TELE: 200201 STRE 38
26 INFORMATION FOR SEQ ID NO: 1:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 142 amino acids
29 TYPE: amino acid
30 TOPOLOGY: linear
31 MOLECULE TYPE: protein
32
33 US 09-943 543 1
34
35 Query Match: 61.1% Score 683; DB 1; Length 142;
36 Best Local Similarity 85.9%; Prod. No. 2,36-69;
37 Matches 127; Conserved 147; Mismatches 7; Indels 0; Gaps 0;
38
39 QY 57 LHHHLLHKKKQYCTGPHOILPNSVGGTFRQHSLEPTISVAVGLISRGVDSG 116
40 1 LHHHLLHKKKQYCTGPHOILPNSVGGTFRQHSLEPTISVAVGLISRGVDSG 60
41
42 QY 117 LVLGMDKGVASSTLSLSTFRLQETLAKRTYGGNLYKREYGEPEFVALNKETPR 176
43 1 LVLGMDKGVASSTLSLSTFRLQETLAKRTYGGNLYKREYGEPEFVALNKETPR 120
44
45 DB 61 LVLGMDKGVASSTLSLSTFRLQETLAKRTYGGNLYKREYGEPEFVALNKETPR 120
46
47 QY 177 LFAKSRKQKTFHFLPRVDPREVLYKQLMY 210
48 1 LFAKSRKQKTFHFLPRVDPREVLYKQLMY 172
49
50 DB 121 LFAKSRKQKTFHFLPRVDPREVLYKQLMY 172
51
52 RESULT 60
53 US 09-943 915 42
54 Sequence 42; Application US/09/94 915
55 Patent No. 590170
56
57 GENERAL INFORMATION:
58 APPLICANT: Hook, No. 59017092PK1
59 APPLICANT: Martin, Frank
60 APPLICANT: Dantoko, Dimity
61 TITLE OF INVENTION: A FIBROBLAST GROWTH FACTOR
62 NUMBER OF SEQUENCES: 4
63 CORRESPONDENCE ADDRESS:
64 ADDRESSEE: Aaron Inc.
65 STREET: 1840 Dwyerland Drive
66 CITY: Thousand Oaks
67 STATE: California
68 COUNTRY: USA
69 ZIP: 91320 1789
70
71 COMPUTER READABLE FORM:
72 MEDIUM TYPE: floppy disk
73 COMPUTER: IBM pc compat 100
74 OPERATING SYSTEM: PC DOS/MS DOS
75 SOFTWARE: Patout In Release #1.0, Version #1.30
76
77 CURRENT APPLICATION DATA:

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```

1 APPLICATION NUMBER: US/09/943 915
2 FILING DATE:
3 CLASSIFICATION: 435
4 AGENT/AGENT INFORMATION:
5 NAME: MURZA, Richard J.
6 REGISTRATION NUMBER: 27 657
7 REFERENCE/PROJECT NUMBER: A-469
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: 805,447,4112
10 TELEFAX: 805,447,1090
11 INFORMATION FOR SEQ ID NO: 42:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 173 amino acids
14 TYPE: amino acid
15 STRANDNESS: single
16 TOPOLOGY: linear
17 MOLECULE TYPE: protein
18
19 US-09-943-915-42
20
21 Query Match: 59.98% Score 670; DB 2; Length 173;
22 Best Local Similarity 73.5%; Prod. No. 8,80-68;
23 Matches 119; Conserved 22; Mismatches 19; Indels 2; Gaps 1;
24
25 QY 49 KQACAAQAMHGLLRKQYCTGPHOILPNSVGGTFRQHSLEPTISVAVGLY 108
26 1 KQACAAQAMHGLLRKQYCTGPHOILPNSVGGTFRQHSLEPTISVAVGLY 70
27
28 DB 13 KQSD-TDFHKKRLRRQYCTGPHOILPNSVGGTFRQHSLEPTISVAVGLY 70
29
30 QY 109 STKGVDSGLVGNRRGELLSKLLDPSVFKQDTLNRGTFVAGTLYKHSRSPGYVA 168
31 1 STKGVDSGLVGNRRGELLSKLLDPSVFKQDTLNRGTFVAGTLYKHSRSPGYVA 140
32
33 DB 71 STKGVDSGLVGNRRGELLSKLLDPSVFKQDTLNRGTFVAGTLYKHSRSPGYVA 140
34
35 QY 169 LNRGTPVDSKSRKQKTFHFLPRVDPREVLYKQLMY 210
36 1 LNRGTPVDSKSRKQKTFHFLPRVDPREVLYKQLMY 172
37
38 DB 131 LNRGTPVDSKSRKQKTFHFLPRVDPREVLYKQLMY 172
39
40 Search completed: April 11, 2002, 09:53:40
41 Job time: 51 sec

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XX The sequence is rat fibroblast growth factor 20, FGF 20. The FGF
 XX polypeptides and nucleic acids encoding them are useful for providing
 XX trophic support for cells in a patient, especially a patient with
 XX Parkinson's disease, and FGF-20 is additionally used to treat patients
 XX with conditions of the substantia nigra. The polypeptides and nucleic
 XX acids are useful for alleviating human brain conditions by slowing
 XX dopaminergic neurons, restoring function of, or increasing the number of,
 XX dopaminergic neurons. The polypeptides and nucleic acids also
 XX are useful for alleviating cardiac associated disease by slowing
 XX degeneration of or restoring or maintaining normal function of the
 XX structure of cardiac, where the disease is osteoporosis, Crohn's
 XX syndrome, Meniere's disease, Peutz-Jeghers syndrome, diabetes associated
 XX hearing loss, congenital malformations, autoimmune disease-related
 XX hearing loss, age related hearing loss, deafness associated with lack
 XX of FGF receptor and ischemia related hearing disturbance, other
 XX diseases thought to be amenable to FGF therapeutic activity include
 XX neuro-degenerative diseases, tendonitis, wound healing, stroke and
 XX ischemia. The polypeptides can be used to screen for agonists and
 XX and antagonists. Epitope binding fragments of the FGF-20 polypeptides can be
 XX used to raise anti FGF-20 antibodies.

XX Sequence: 212 AA:

Query Match: 96.1%, Score: 1927, E: 1e-222, Length: 212;
 Best Local Similarity: 95.4%; Prod. No. 1067
 Matches: 201; Conservative: 42; Mismatches: 73; Indels: 0; Gaps: 0;

1 MATAVAGAPGAGLGGVSHPLLPACGKPPPLGERSAERSARKGACAAAL 60
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 1 MAPGCGATGQGLGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGGKGGG 60
 61 MGLTLPKQVYKRGHGLGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGG 120
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 61 MGLTLPKQVYKRGHGLGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGG 120
 61 MGLTLPKQVYKRGHGLGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGG 120
 121 MGLTLPKQVYKRGHGLGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGG 180
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 121 MGLTLPKQVYKRGHGLGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGG 180
 121 MGLTLPKQVYKRGHGLGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGG 180
 181 SKLQKPLGLGPPGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGG 211
 181 SKLQKPLGLGPPGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGG 211

RESULT 5

AAW11548

AAW11548

17 SEP 1997 (first entry)

XX Amino acid sequence of chicken FGF9 encoded by FGF9PPT-80.

XX Mouse chikoen fibroblast growth factor 9; FGF9; detection;

XX fibroblast growth factor receptor 3; FGFR3; cartilage repair;

XX bone repair; antagonist; anti FGF9 and body; endothelium;

XX solitary hereditary exostosis; multiple hereditary exostosis;

XX hallux valgus deformity; arthroplasty; synovial chondromatosis.

XX Gallus domesticus.

XX Key: Locat ion/Qual ities

XX Misc difference 216

XX Note: *Given in the specification as 2, encoded by 15A*

XX W09041543 A1.

XX 27 DEC 1996.

XX 12 JUN 1996. W09041543 A1.

XX 12-JUN-1995; 9505-0000137.
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX Yayan A:
 XX WPI: 1997-065215/06.
 XX N-PSDB: AAT58531.
 XX Medical and diagnostic use of fibroblast growth factor 9 - and
 XX recombinant fibroblast growth factor 9 DNA
 XX Claim 13; Fig 2; 32pp; English.

XX The sequences given in AAW11547 48 represent mouse and chicken
 XX fibroblast growth factor 9 (FGF9) respectively. FGF9 may be used in the
 XX method of the invention for detecting fibroblast growth factor receptor 3
 XX (FGFR3) in a sample of tissue. The method comprises contacting the
 XX sample or tissue with FGF9, allowing formation of receptor-ligand pairs,
 XX and detecting any FGFR3-FGF9 pairs. Compositions containing FGF9 can
 XX be used to increase FGFR3 activity, esp. to stimulate cartilage or bone
 XX repair. Compositions containing FGF9 and agonists or FGF9 binding agents
 XX (e.g., anti-FGF9 antibodies) can be used to treat diseases caused by an
 XX excess of FGF9 or overactivity of FGFR3, esp. multiple or solitary
 XX hereditary exostosis, hallux valgus deformity, arthroplasty, synovial
 XX chondromatosis and endochondromas.

XX Sequence: 220 AA:

Query Match: 69.6%; Score: 778.5; E: 1e-183, Length: 220;
 Best Local Similarity: 71.6%; Prod. No. 4676;
 Matches: 151; Conservative: 19; Mismatches: 32; Indels: 9; Gaps: 4;

1 MATAVAGAPGAGLGGVSHPLLPACGKPPPLGERSAERSARKGACAAAL 57
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 2 MGLTLPKQVYKRGHGLGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGG 61
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 58 AMLHGLKRGHGLGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGGKGGG 117
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 62 MGLTLPKQVYKRGHGLGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGG 121
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 122 MGLTLPKQVYKRGHGLGQVSHSLTPGKPPPLGKGGGKGGGKGGGKGGG 181
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 178 GAKSKRGKPPPLGERSAERSARKGACAAAL 208
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 182 GAKSKRGKPPPLGERSAERSARKGACAAAL 212

RESULT 6

AAK27207

AAK27207

20 MAY 1998 (first entry)

XX Glia activating factor #1.

XX GAF: stimulates glial cell growth; cerebral nerve cell lesions;

XX cerebral edema; Alzheimer's disease; senile dementia;

XX diabetic neuropathy; stimulates fibroblasts; burns; wounds; ulcers;

XX stimulates megakaryocytes; increase platelets; haematopoietic cells;

XX immunocompetent cells; vascular smooth muscle cells; bone fractures;

XX osteogenesis promoting activity; osteoporosis; cerebral tumours;

XX stimulates cultured cells.

XX Homo sapiens.

XX EP504297-A.

XX alpha activating factor: GAF; first time; detection; antibody; cancer;
 KW osteoporosis; platelets; hepatocellular carcinoma; anti-tumor agent;
 XX
 OS Hemo saphrons;
 XX
 EN EPO08046. A;
 XX
 EN 04 ADJ: 1994;
 XX
 PE 18 MAR: 1994; 94EP-0120491;
 XX
 PE 22 MAR: 1994; 94EP-0342100;
 PE 23 ADJ: 1994; 94EP-0207719;
 XX
 EN (TAKA) TAKARA CHEM IND LTD;
 XX
 EN Kurokawa T., Kuroshima K., Sasaki T., Yoshitani S;
 XX
 EN WPI: 1994-242006/30;
 XX
 PT New alpha activating factor polypeptide and antibodies - for use
 PT in detection, purification and treatment of diseases, e.g. as
 PT anti-tumor or platelet increasing agents;
 XX
 EN Disclosure: Page 40-41; 80pp; English;
 XX
 CC The alpha activating factor (GAF) polypeptides (See AAR56503-56511) can
 CC be used as platelet increasing agents, osteoporosis promoting
 CC agents or for treating cerebral nervous diseases or hepatopathy such
 CC as hepatic cirrhosis. They can also be used to treat cancer when
 CC used alongside an anti-tumor agent. Antibodies directed against the
 CC GAF polypeptides can be used for detecting or determining a
 CC biochemical activity of a GAF polypeptide or for purifying a GAF
 CC polypeptide. The antibodies, which also neutralise the cell growth
 CC activity of GAF, can be used as anti-tumor agents;
 XX
 EN Sequence: 208 AA;
 XX
 QY Query Match: 69, 38; Score 774.5; DB 15; Length 208;
 QY Host Local Similarity: 70, 68; Pred. No. to 74;
 QY Matches: 149; Conservation: 23; Mismatch: 40; Indels: 9; Gaps: 4;
 QY
 DB 1 MARIATVGGTGLDGLDGVNSHPIAPVAGKRPDLAGEKRSAAERSAAG--GPAVAAL 57
 DB 1 mapqvevny/zyjyap p/-nnyf/pv -deplfslthlqpsr--anlppqvrdl 54
 QY
 DB 58 AHHHGLRRKQRYKRPFHGLIPDSVGRKQUNSLVGLHLSVAVGLVSLRGVNSL 117
 DB 55 dhkqitrrqlyetrbhclpogrlqptkbsrtatlelslavqlsslrqvsdl 114
 QY
 DB 118 YAGMNGKGLVGSERKLSFSLFRKQPTENMYRYSNRYKRGDTPGKAYVNAKMDGTPRD 177
 DB 115 ylgmngkvl/ygsrklsfslfrkqptenmyr/snrykrgdtpgkayvna/mkdgtp 174
 QY
 DB 178 GASKRKQKCTHPLPKVDPKRVKRYKQAL 208
 DB 175 gtttkrkqktlplpkvdpkryvrykqdl 205
 QY
 DB 13 MAY: 1996 (first entry)
 XX
 DE Fibroblast growth factor 9; FGF 9;
 XX
 KW Compound: Fibroblast growth factor; FGF; cytototoxic; supporting; eye;
 KW cell proliferation; regulation; prolydase; corneal clouding; cancer;
 XX

KW psoriasis; rheumatoid arthritis;
 XX
 OS Hemo saphrons;
 XX
 EN W09524928 A2;
 XX
 EN 21 SEP: 1995;
 XX
 EN 15-MAR-1995; 95WO-0504448;
 XX
 EN 15-MAR-1994; 94US-0214447;
 EN 15-MAR-1994; 94US-0214446;
 XX
 EN (PRIZ) PRIZM FIBRA INC;
 XX
 EN Baird JA, Houston JL, Nova MD, Sosnowski BA;
 XX
 EN WPI: 1995-336820/43;
 XX
 PT New conjugates of growth factor receptor ligand and targeted agent
 PT - partic, DNA or cytotoxin, used to control cell proliferation in
 PT the eye, e.g. to prevent growth of pterygia and corneal clouding
 XX
 PS Claim 33; Page 148; 204pp; English;
 XX
 CC AAR0776-84 are fibroblast growth factors (FGF) FGF-1 to FGF-9
 CC respectively. DNA encoding these fibroblast growth factors can be
 CC used to create an FGF/saporin fusion protein. DNA encoding such fusion
 CC proteins are useful for targeting saporin (a cytotoxin) to a cell
 CC carrying the FGF receptor. Targeted agents (TA) other than saporin
 CC which may be used include in partic, DNA encoding a therapeutic protein,
 CC an enzyme, DNA or other cytotoxic agent. The linker sequence within the
 CC fusion protein may increase serum stability or intracellular
 CC availability of the TA. The conjugates of the invention are used to
 CC inhibit cell proliferation in cells carrying the particular growth
 CC factor receptor; also when TA is DNA it can be used to deliver this
 CC to cells (for gene therapy). A specific application is to prevent
 CC excessive proliferation of epithelial cells, fibroblasts and
 CC keratinocytes in the anterior eye after surgical removal of pterygia
 CC recurrence of pterygia after surgical removal and corneal clouding after
 CC trabeculectomy after glaucoma surgery and corneal clouding after
 CC excimer laser treatment. Other conditions which may be treated include
 CC tumors, psoriasis, psoriasis, psoriasis, psoriasis, psoriasis, psoriasis,
 CC complications, Kaposi's sarcoma and rheumatoid arthritis;
 XX
 EN Sequence: 208 AA;
 XX
 QY Query Match: 69, 38; Score 774.5; DB 15; Length 208;
 QY Host Local Similarity: 70, 68; Pred. No. to 74;
 QY Matches: 149; Conservation: 23; Mismatch: 40; Indels: 9; Gaps: 4;
 QY
 DB 1 MARIATVGGTGLDGLDGVNSHPIAPVAGKRPDLAGEKRSAAERSAAG--GPAVAAL 57
 DB 1 mapqvevny/zyjyap p/-nnyf/pv -deplfslthlqpsr--anlppqvrdl 54
 QY
 DB 58 AHHHGLRRKQRYKRPFHGLIPDSVGRKQUNSLVGLHLSVAVGLVSLRGVNSL 117
 DB 55 dhkqitrrqlyetrbhclpogrlqptkbsrtatlelslavqlsslrqvsdl 114
 QY
 DB 118 YAGMNGKGLVGSERKLSFSLFRKQPTENMYRYSNRYKRGDTPGKAYVNAKMDGTPRD 177
 DB 115 ylgmngkvl/ygsrklsfslfrkqptenmyr/snrykrgdtpgkayvna/mkdgtp 174
 QY
 DB 178 GASKRKQKCTHPLPKVDPKRVKRYKQAL 208
 DB 175 gtttkrkqktlplpkvdpkryvrykqdl 205
 QY
 DB 13 MAY: 1996 (first entry)
 XX
 DE Fibroblast growth factor 9; FGF 9;
 XX
 KW Compound: Fibroblast growth factor; FGF; cytototoxic; supporting; eye;
 KW cell proliferation; regulation; prolydase; corneal clouding; cancer;
 XX

XX	AAW75/19.	
XX	07 1998 1998 (first entry)	
XX		
XX	Fibroblast growth factor 9.	
XX	Fibroblast growth factor-9; FGF-9; murine; protein; covalent;	
KW	heparin; thrombosis; thrombocytopoietic; epithelial disorders;	
KW	human; thrombosis.	
XX		
XX	Human sequences.	
XX		
XX	Key: Location/qualifiers	
XX		
XX	Misc difference 136	
XX	/note: "Phe-136 is replaced by another amino acid	
XX	acid (Glu-136), preferably Ala, Phe, Ser,	
XX	Gly, Met, Asn or Tyr, especially Ala, Gly	
XX	or Ser"	
XX		
XX	Misc difference 137	
XX	/note: "Glu-137 may be replaced by another amino	
XX	acid (Glu-137), preferably Ala, Gly or Ser"	
XX		
XX	Misc difference 143	
XX	/note: "Asn-143 may be replaced by another amino	
XX	acid (Glu-143), preferably Ala, Phe, Ser,	
XX	Gly, Met, Asn or Tyr, especially Ala, Gly	
XX	or Ser"	
XX		
XX	Misc difference 146	
XX	/note: "Asn-146 may be replaced by another amino	
XX	acid (Glu-146), preferably Ala, Phe, Ser,	
XX	Gly, Met, Asn or Tyr, especially Ala, Gly	
XX	or Ser"	
XX		
XX	W09849466. A2.	
XX		
XX	11 SEP 1998.	
XX		
XX	03 MAR 1998; 98W014000878.	
XX		
XX	03 MAR 1997; 97US-0040785.	
XX		
XX	(EISA) EISA1 010 111.	
XX		
XX	Kalyanaraman R, Kawai T, Zhu H;	
XX		
XX	W01: 1998 496843/42.	
XX		
XX	Fibroblast growth factor molecule and DNA having reduced receptor	
XX	binding and able to bind heparin, useful for treating and regulating	
XX	heparin related disorders e.g. thrombosis	
XX		
XX	Discovered; Page 59 60; 71pp; English.	
XX		
XX		
XX	This is the amino acid sequence of fibroblast growth factor-9	
XX	(FGF-9), a claimed DNA molecule of the invention encodes FGF molecule	
XX	polypeptides (see AWW75/11 20) that show reduced FGF receptor binding	
XX	activity but which retain the ability to bind heparin. For FGF-9,	
XX	amino acid residues 146, 143 and 146 are preferably replaced by	
XX	other amino acid residues, with an optional further replacement of	
XX	the Glu-137 residue. The molecule may be further modified by	
XX	replacement of the Cys residues to reduce aggregation. The molecule	
XX	is obtained by site-specific or site-directed mutagenesis of FGF-9	
XX	RNA, incorporation of the mutated DNA into a vector and expression	
XX	in host cells. The FGF molecules are used to treat heparin-related	
XX	disorders, such as excessive bleeding, induced by heparin,	
XX	epithelial disorders and heparin-associated thrombocytopoia and	
XX	thrombosis. They may also be used for drug design.	
XX		
XX	Sequence: 208 AA;	

[illegible]

20-MAY-1999; 9905-0135166.
 XX (JEMMA-) HUMAN GENE: SEC1 INC.
 XX
 P1 Alderson K, Greene JM, Melder K, Inan EK, Dillon PJ.
 P1 WPI: 2001-025137703.
 XX
 P1 New isolated nucleic acid encoding human fibroblast growth factor 14
 P1 for diagnosis, prevention, and treatment of: immune disorders; cancer
 P1 and infectious diseases
 XX
 PS disclosure: Page 260-261; 268pp; English.
 XX
 CC The present invention provides the protein and coding sequences for human
 CC fibroblast growth factor 14 (FGF-14). These sequences can be used in the
 CC diagnosis and treatment of infections, cancer, autoimmune disorders,
 CC hyperproliferative disorders, cardiovascular disorders and neurological
 CC diseases, to prevent angiogenesis and to aid wound healing.
 XX
 SS Sequence: 208 AA.

Query Match: 69.4%; Score 774.5; 18 22; Length 208;
 Post Local Similarity: 70.6%; Prot. No. 16 74;
 Matches: 149; Conservative: 23; Mismatches: 30; Indels: 9; Gaps: 4;

QY 1 MAPLAENVNHLGGITGLQVNSHLLPPAHERPLIDRESAARSAAG--GRPAAL 57
 DB 1 maplaenvnlygghlqgvnsllppaherplidresaaarsaag--grpaal 54
 QY 58 AHHLILRRKQVIERIGRHQILPNSVSGTHQHSLEFLETSVAVGVASRGVDSL 117
 DB 58 dhlilrrkqvierigrhqlpnsvsgthqhsleflfetsvavgvastrgvdsll 114
 QY 119 YFSGGFGNLSZLALZLALZLALZLALZLALZLALZLALZLALZLALZL 177
 DB 119 yfsggfgnlszalnslzalnslzalnslzalnslzalnslzalnslzalnsl 174
 QY 115 yfsggfgnlszalnslzalnslzalnslzalnslzalnslzalnslzalnsl 174
 DB 115 yfsggfgnlszalnslzalnslzalnslzalnslzalnslzalnslzalnsl 174
 QY 179 GABSEPRKRPPIPPVPPVPPVPPVPPVPPVPPVPPVPPVPPVPPVPPV 205
 DB 179 gabsprkrppippvppvppvppvppvppvppvppvppvppvppvppv 205

RESULT: 21

AAB50295

ID AAB50295 standard; Protein: 208 AA.

XX AAB50295;

DE 20-MAR-2001 (first entry)

DE Human fibroblast growth factor 9 SEQ ID NO: 4.

XX Human: fibroblast growth factor 11; FGF-11; cancer; autoimmune disorder;

KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;

KW wound healing; neurological disease; infection.

OS Homo sapiens.

PN W0200071715-A1.

PN 30 NOV 2000.

PE 16-MAY 2000; 2000W-0513441.

PR 21-MAY-1999; 9905-0135524.

PA (JEMMA-) HUMAN GENE: SEC1 INC.

PI Kosen CA, Alderson K, Melder K, Duan RD, Hu J;
 WPI: 2001-016408702.

XX polynucleotide encoding human fibroblast growth factor 11, useful in
 P1 the diagnosis, treatment and prevention of cancer; immune disorders,
 P1 cardiovascular disorders and neurological diseases
 XX
 PS disclosure: Page 268; 268pp; English.

CC The present invention provides the protein and coding sequences for human
 CC fibroblast growth factor 11 (FGF-11). These sequences can be used in the
 CC diagnosis and treatment of infections, cancer, autoimmune disorders,
 CC hyperproliferative disorders, cardiovascular disorders and neurological
 CC diseases, to prevent angiogenesis and to aid wound healing.

SS Sequence: 208 AA.

Query Match: 69.4%; Score 774.5; 18 22; Length 208;
 Post Local Similarity: 70.6%; Prot. No. 16 74;
 Matches: 149; Conservative: 23; Mismatches: 30; Indels: 9; Gaps: 4;

QY 1 MAPLAENVNHLGGITGLQVNSHLLPPAHERPLIDRESAARSAAG--GRPAAL 57
 DB 1 maplaenvnlygghlqgvnsllppaherplidresaaarsaag--grpaal 54
 QY 58 AHHLILRRKQVIERIGRHQILPNSVSGTHQHSLEFLETSVAVGVASRGVDSL 117
 DB 58 dhlilrrkqvierigrhqlpnsvsgthqhsleflfetsvavgvastrgvdsll 114
 QY 119 YFSGGFGNLSZLALZLALZLALZLALZLALZLALZLALZLALZLALZL 177
 DB 119 yfsggfgnlszalnslzalnslzalnslzalnslzalnslzalnslzalnsl 174
 QY 115 yfsggfgnlszalnslzalnslzalnslzalnslzalnslzalnslzalnsl 174
 DB 115 yfsggfgnlszalnslzalnslzalnslzalnslzalnslzalnslzalnsl 174
 QY 179 GABSEPRKRPPIPPVPPVPPVPPVPPVPPVPPVPPVPPVPPVPPVPPV 205
 DB 179 gabsprkrppippvppvppvppvppvppvppvppvppvppvppvppv 205

RESULT: 22

AAB50710

ID AAB50710 standard; Protein: 208 AA.

XX AAB50710;

DE 20-MAR-2001 (first entry)

DE Human fibroblast growth factor 9 SEQ ID NO: 8.

XX Human: fibroblast growth factor 11; FGF-11; cancer; autoimmune disorder;

KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;

KW wound healing; neurological disease; infection.

OS Homo sapiens.

PN W0200071715-A1.

PN 30 NOV 2000.

PE 18-MAY 2000; 2000W-0514573.

PR 21-MAY 1999; 9905-0145523.

PA (JEMMA-) HUMAN GENE: SEC1 INC.

PI Kosen CA, Alderson K, Melder K, Inan EK, Dwyane JD;
 WPI: 2001-016451702.

XX polynucleotide encoding human fibroblast growth factor 10, useful in
 P1 the diagnosis, treatment and prevention of cancer; immune disorders,
 P1 cardiovascular disorders and neurological diseases
 XX
 PS disclosure: Page 266-267; 275pp; English.

[illegible]

XX	RESIDUE 45
XX	AAV05474
XX	AAV05474 standard, protein, 207 AA
XX	AAV05474:
XX	07 JUL 1999 (first entry)
XX	
XX	Human FGF-16 protein sequence.
XX	
XX	FGF-16, fibroblast growth factor-16, growth therapy, cell therapy, FGF16, hepatocyte growth, proliferation stimulation, liver disorder, cirrhosis, fulminant liver failure, viral hepatitis, detection.
XX	
XX	Human sapropterin
XX	W0910428 A1
XX	15 APR 1999
XX	
XX	28 APR 1998
XX	03 OCT 1997
XX	970US 0943759
XX	
XX	(AMTE) AMTEEN INC.
XX	
XX	Arakawa T, Danilovsko MD, Toch N, Martin FH
XX	
XX	WPI: 1999-264099/22
XX	USPB: AAX00528
XX	
XX	New fibroblast growth factor useful for treating liver conditions
XX	
XX	claim 1: Fig 6; 87pg; English.
XX	
XX	This sequence is the human fibroblast growth factor-16 (FGF-16) of the invention. Vectors containing nucleic acid sequences that encode FGF-16 are useful in gene and cell therapy by in vivo transduction, and for production of recombinant FGF-16. Treatment of hepatocellular carcinoma in vitro or in vivo stimulates their growth and proliferation. FGF-16 treated hepatocellular carcinomas are used to treat a liver disease or disorder in the host organism, e.g., cirrhosis; fulminant liver failure; or damage caused by viral hepatitis and/or toxins. FGF-16 is also used to raise antibodies useful for in vitro or in vivo detection of FGF-16. FGF-16 acts specifically on hepatocytes.
XX	Sequence: 207 AA:

[illegible]

DB	115	140	145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	530	535	540	545	550	555	560	565	570	575	580	585	590	595	600	605	610	615	620	625	630	635	640	645	650	655	660	665	670	675	680	685	690	695	700	705	710	715	720	725	730	735	740	745	750	755	760	765	770	775	780	785	790	795	800	805	810	815	820	825	830	835	840	845	850	855	860	865	870	875	880	885	890	895	900	905	910	915	920	925	930	935	940	945	950	955	960	965	970	975	980	985	990	995	1000
Q7	179	184	189	194	199	204	209	214	219	224	229	234	239	244	249	254	259	264	269	274	279	284	289	294	299	304	309	314	319	324	329	334	339	344	349	354	359	364	369	374	379	384	389	394	399	404	409	414	419	424	429	434	439	444	449	454	459	464	469	474	479	484	489	494	499	504	509	514	519	524	529	534	539	544	549	554	559	564	569	574	579	584	589	594	599	604	609	614	619	624	629	634	639	644	649	654	659	664	669	674	679	684	689	694	699	704	709	714	719	724	729	734	739	744	749	754	759	764	769	774	779	784	789	794	799	804	809	814	819	824	829	834	839	844	849	854	859	864	869	874	879	884	889	894	899	904	909	914	919	924	929	934	939	944	949	954	959	964	969	974	979	984	989	994	999	1000								
DB	126	131	136	141	146	151	156	161	166	171	176	181	186	191	196	201	206	211	216	221	226	231	236	241	246	251	256	261	266	271	276	281	286	291	296	301	306	311	316	321	326	331	336	341	346	351	356	361	366	371	376	381	386	391	396	401	406	411	416	421	426	431	436	441	446	451	456	461	466	471	476	481	486	491	496	501	506	511	516	521	526	531	536	541	546	551	556	561	566	571	576	581	586	591	596	601	606	611	616	621	626	631	636	641	646	651	656	661	666	671																																																																

RES01.1	36	
AAV58429		
110	AAV58429 standard; Protein; 207 AA.	
XX		
AC	AAV58429;	
XX		
DT	27-MAR-2000 (first entry)	
XX		
OE	Human fibroblast growth factor FGF-16.	
XX		
KM	Fibroblast growth factor: FGF-16; human; hepatocyte proliferation;	
XX	hepatolipotic; liver disorder; viral hepatitis; cirrhosis; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
PN	U55998170-A.	
XX		
PD	07-DEC-1999.	
XX		
PI	03-OCT-1997; 97US-094915.	
XX		
PK	03-OCT-1997; 97US-094915.	
XX		
PA	(AMGE-) AMGEN INC.	
XX		
PI	Arakawa T, Itoh R, Danilenko DM, Martin FH;	
XX		
DK	WPI: 2000-085497/07.	
DR	N-PSDB: AAV55791.	
XX		
PT	Fibroblast growth factor family polypeptide which stimulates	
PT	proliferation and growth of hepatocytes is useful for treating hepatic	
PT	disorders.	
XX		
PS	Claim 1; Fig 6A-B; 33pp; English.	
XX		
XX		
CC	This sequence represents human fibroblast growth factor-16 (FGF-16).	
CC	FGF-16 has hepatocyte proliferation and growth activity, and	
CC	increases hepatic production of triglycerides and serum proteins (e.g.,	
CC	albumin). FGF-16, nucleic acids and/or proteins may be used for	
CC	stimulating the proliferation and development of hepatocytes both in	
CC	vitro and in vivo. The isolated nucleic acid molecules may be used	
CC	directly in cell or gene therapy applications to treat or prevent liver	
CC	disorders, including hepatic cirrhosis, fulminant liver failure, damage	
CC	caused by acute viral hepatitis and toxic insult to the liver.	
XX		
SO	Sequence 207 AA;	

[illegible]

09 65 BRQJYVQI QZBQJLHFGSVQTHQJHSTFHLLEISVAVQIYQIBQVQZLYLZQI 122
 1 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 10 86 HQSLPQVQI QZBQJLHFGSVQTHQJHSTFHLLEISVAVQIYQIBQVQZLYLZQI 144
 1 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 09 123 BRQJYVQI QZBQJLHFGSVQTHQJHSTFHLLEISVAVQIYQIBQVQZLYLZQI 160
 1 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 10 145 BRQJYVQI QZBQJLHFGSVQTHQJHSTFHLLEISVAVQIYQIBQVQZLYLZQI 204
 1 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 09 180 BRQJYVQI QZBQJLHFGSVQTHQJHSTFHLLEISVAVQIYQIBQVQZLYLZQI 203
 1 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 10 205 BRQJYVQI QZBQJLHFGSVQTHQJHSTFHLLEISVAVQIYQIBQVQZLYLZQI 226
 1 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

Search completed: April 11, 2002, 09:54:21
 Job time: 42 sec

QY 1 MAPLAEVCPRLGGPPELGGVSGSHLLPRAPEPRPLIGERKSAERSARG---GRGAOL 57
 DB 1 MAHLAEVGNFVGQAVN---PEGVNVPRLV---DSPVLLSDHGGSE---AGSLPRGPVTL 54
 QY 56 ARIHGLPRRQYCRKQCHPHGLIIPDSVQCRKQCHSLGLLEPISVAVGLVSRGVSGL 117
 DB 55 DILKGLRRKQYCRKQCHPHGLIIPDSVQCRKQCHSLGLLEPISVAVGLVSRGVSGL 114
 QY 118 YIGMNEFCRLYGEELTSEGLPEPRQENNYSSNYKQDCTQRYVALAKDGTTRD 177
 DB 115 YIGMNEFCRLYGEELTSEGLPEPRQENNYSSNYKQDCTQRYVALAKDGTTRD 174
 QY 178 GAPSRRQKPRPLPRVPPVPPVPPVKKLL 208
 DB 175 YPRPRKPRPLPRVPPVPPVPPVKKLL 205

RESULT 6

Fibroblast growth factor 16 - human

CSpecies: Homo sapiens (man)

CDate: 16-Jul-1999 #sequence_revision 16 Jul 1999 #text_change 21-Jul-2000

CAccession: J05941

P.Miyata, A. Y. Kishida, M. Matsumoto, F. H. R. de Almeida, N. A. de Almeida, E. Yamamoto, S. Miyamoto, Biochem. Biophys. Res. Commun. 243, 148-152, 1998

AtTitle: Structure and expression of a novel member, FGF-16, of the fibroblast growth factor

AtReference number: J05941, PMID: 9819888

AtAccession: J05941

AtStatus: preliminary

AtMolecule type: DNA

AtCross-reference: 1797 MIV

AtCross-reference: DBM:AB005611; NID:42911147; PDB:1MAA2496.1; PDB:42911170

CSuperfamily: fibroblast growth factor

Query Match 53.1% Score 709.57 DB 2 Length 207
 Best Local Similarity 63.0% Prod. No. 976 59
 Matches 141 Conservative 27 Mismatches 40 Indels 11 Gaps 4

QY 4 LAAGVQFLGSL---GAGVQVSHPLIPRAGPRPLIGERKSAERKSAERGAAGA 58
 DB 1 MAEVGVFASLMDLDEPSSIGN---VPLASPCPLNERLQGERKQGRSP 99FA 54
 QY 59 HLMGLRRKQYCRKQCHPHGLIIPDSVQCRKQCHSLGLLEPISVAVGLVSRGVSGL 118
 DB 55 HLMGLRRKQYCRKQCHPHGLIIPDSVQCRKQCHSLGLLEPISVAVGLVSRGVSGL 114
 QY 118 YIGMNEFCRLYGEELTSEGLPEPRQENNYSSNYKQDCTQRYVALAKDGTTRD 177
 DB 115 YIGMNEFCRLYGEELTSEGLPEPRQENNYSSNYKQDCTQRYVALAKDGTTRD 174
 QY 178 GAPSRRQKPRPLPRVPPVPPVPPVKKLL 208
 DB 175 YPRPRKPRPLPRVPPVPPVPPVKKLL 206

RESULT 7

Fibroblast growth factor 16 - rat

CSpecies: Rattus norvegicus (Norway rat)

CDate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

CAccession: J05940

R.Miyata, A. Y. Kishida, M. Matsumoto, F. H. R. de Almeida, N. A. de Almeida, E. Yamamoto, S. Miyamoto, Biochem. Biophys. Res. Commun. 243, 148-152, 1998

AtTitle: Structure and expression of a novel member, FGF-16, of the fibroblast growth factor

AtReference number: J05940, PMID: 9819888

AtAccession: J05940

AtStatus: preliminary

AtMolecule type: DNA

AtCross-reference: 1797 MIV

AtCross-reference: DBM:AB005611; NID:42911147; PDB:1MAA2496.1; PDB:42911170

CSuperfamily: fibroblast growth factor

Query Match 64.1% Score 705.57 DB 2 Length 207
 Best Local Similarity 62.7% Prod. No. 1786 58
 Matches 134 Conservative 28 Mismatches 40 Indels 11 Gaps 4

QY 4 LAAGVQFLGSL---GAGVQVSHPLIPRAGPRPLIGERKSAERKSAERGAAGA 58
 DB 1 MAEVGVFASLMDLDEPSSIGN---VPLASPCPLNERLQGERKQGRSP 99FA 54
 QY 59 HLMGLRRKQYCRKQCHPHGLIIPDSVQCRKQCHSLGLLEPISVAVGLVSRGVSGL 118
 DB 55 HLMGLRRKQYCRKQCHPHGLIIPDSVQCRKQCHSLGLLEPISVAVGLVSRGVSGL 114
 QY 118 YIGMNEFCRLYGEELTSEGLPEPRQENNYSSNYKQDCTQRYVALAKDGTTRD 177
 DB 115 YIGMNEFCRLYGEELTSEGLPEPRQENNYSSNYKQDCTQRYVALAKDGTTRD 174
 QY 178 GAPSRRQKPRPLPRVPPVPPVPPVKKLL 208
 DB 175 YPRPRKPRPLPRVPPVPPVPPVKKLL 206

RESULT 8

Fibroblast growth factor 4 - chicken

CSpecies: Gallus gallus (chicken)

CDate: 14-Sep-1996 #sequence_revision 14-Sep-1996 #text_change 17-Mar-2000

CAccession: J150588

R. Belmont, R. K. Kiefer, P. G. Guller, S. D. Johnson, D. J. Mason, J. Development 121, 1399-1410, 1995

AtTitle: Multiple roles for FGF-4 during chick limb development

AtReference number: J150588, PMID: 9540912

AtAccession: J150588

AtStatus: preliminary; translated from cDNA (700b)

AtMolecule type: mRNA

AtReference: 1220 RDB

AtCross-reference: DBM:427557; NID:424215; PDB:1MAA2496.1; PDB:427557

CSuperfamily: fibroblast growth factor

Query Match 40.6% Score 442.57 DB 2 Length 200
 Best Local Similarity 41.6% Prod. No. 146 47
 Matches 77 Conservative 29 Mismatches 56 Indels 23 Gaps 4

QY 26 LIP---PARRPRPLIGERKSAERKSAERGAAGAHLHGLRRKQYCRKQCHPHGLIIP 81
 DB 1 LIPPRVPAVIAAP---PARRPRPLIGERKSAERKSAERGAAGAHLHGLRRKQYCRKQCHPHGLIIP 81
 QY 82 LIPPRVPAVIAAP---PARRPRPLIGERKSAERKSAERGAAGAHLHGLRRKQYCRKQCHPHGLIIP 81
 DB 62 LIPPRVPAVIAAP---PARRPRPLIGERKSAERKSAERGAAGAHLHGLRRKQYCRKQCHPHGLIIP 81
 QY 140 LIPPRVPAVIAAP---PARRPRPLIGERKSAERKSAERGAAGAHLHGLRRKQYCRKQCHPHGLIIP 81
 DB 122 LIPPRVPAVIAAP---PARRPRPLIGERKSAERKSAERGAAGAHLHGLRRKQYCRKQCHPHGLIIP 81
 QY 192 LIPPRVPAVIAAP---PARRPRPLIGERKSAERKSAERGAAGAHLHGLRRKQYCRKQCHPHGLIIP 81
 DB 182 LIPPRVPAVIAAP---PARRPRPLIGERKSAERKSAERGAAGAHLHGLRRKQYCRKQCHPHGLIIP 81

RESULT 9

Fibroblast growth factor 5 - rat

CSpecies: Rattus norvegicus (Norway rat)

CDate: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

CAccession: S68144

R. Miyata, Y. Yamazaki, M. Itoh, N. Biochem. Biophys. Acta 1306, 11-13, 1996

AtTitle: The rat FGF-5 mRNA variant, pFGF-5, is a novel member of the fibroblast growth factor

AtReference number: S68144, PMID: 9620170

AtAccession: S68144

AtStatus: preliminary; nucleotide acid sequence not shown

C keywords: growth factor; heparin binding

Query Match 22.98; Score 256; DB 1; Length 155;
 Best Local Similarity 66.08; Pred. No. 10-16;
 Matches 63; Conservative 22; Mismatches 54; Indels 46; Gaps 4;
 QY 25 FLTPVACPEPPLIGPPPSAEPSSAPWQPMAMLIHIGILRRKGLYKPTGFH-IGLLPAG 83
 DB 16 FNLDPGNPKKPKL-----LYSGNGHFLRLPAG 44
 QY 64 SVGCTTCGACACCTCTCTSVAVGLVGVGVGSLTQGMKPKPTVQSEKLTSPQLEPQF 143
 DB 45 TVDITKRSDDHQLQLSASVGEVYIKETLQVTLAMQLDGLDGLSGLPTECLLELRL 104
 QY 144 ELAWKELVAGNLYEELTCTEETVA:RLEETTPPEVAFEPSEKPTHTLPQV 195
 DB 105 EENHNYIVLSK-KMAD-KMFWGLKKNKSKKCHFLHVDQNALITCTLEVSID 155

RESULT 29

Keywords: growth factor 4 mouse
 fibroblast growth factor 4 mouse
 N/A alternate names: Transforming protein hst11; transforming protein k-40f; transforming
 C/Species: Mus musculus (house mouse)
 C/Date: 31 Mar 1991 #sequence_revision 31 Mar 1991 #ext_change 17 Mar 2003
 C/Accession: S04741; A57460
 R/Goodrich, S.P.; Smith, R.; Thirumangalakudi, C.; Roberts, G.
 Nucleic Acids Res. 17, 4047-4049, 1989
 A/Title: The mouse homolog of hst/8.101: sequence, genome organization and localization
 A/Reference number: S04741; M010:89296455
 A/Accession: S04741
 A/Molecule type: DNA
 A/Residues: 1-207 (hst-)
 A/Cross-references: GI:814847; EMBL:828756; RDB:472791; EIDN:CAA2967.1; FID:452792
 R/Goodrich, J.M.; Basilico, C.; Goldfarb, R.; Han, O.; Martin, G.R.
 Dev. Biol. 138, 454-463, 1990
 A/Title: Isolation of cDNAs encoding four mouse fGF family members and characterization
 A/Reference number: A57460; M010:90201564
 A/Accession: A57460
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-166; S: 168-202 (hst-)
 A/Cross-references: GI:810642; NID:9194290; PIDN:AAA37619.1; FID:4309247
 C/Comment: best
 A/Comment: best
 C/Superfamily: fibroblast growth factor
 C/Keywords: growth factor; transforming protein

Query Match 22.98; Score 256; DB 1; Length 202;
 Best Local Similarity 47.28; Pred. No. 1-90-16;
 Matches 23; Conservative 23; Mismatches 69; Indels 28; Gaps 7;
 QY 5 AEWGTHLGLHGLDGLVGSILFLPFAERGLLLEKRSAAERSARGLRVAAGLHIGIL 64
 DB 47 ARLA RHWMDL--VAKSLARLVAAQPP---QAAVRSVAD-----YLGLK 77
 QY 65 RRLGLGRI GPHGLLPLPSVQCIKQHSLEGLLETSVAVLVSIRVSNLTLQMN 122
 DB 78 RRLGLGRI NVLTPHGLVLPKRGVHAD-TDGLLPLSPVQGVASTPVAHREFAVS 136
 QY 124 DGLVAGSGLLEETLEKGLTLMVNTVSGNLYKELTGRETVAKRGLTTRKDAKSK 162
 DB 147 SRKGLGVPR LDEKFKGLDRLDGLTAVAT--MMLSKMRETEKQKVS 190
 QY 184 RRLGLGRI PR 194
 DB 194 TRKVTPLAR 201
 RESULT 30
 JH0476

acidic fibroblast growth factor - pig (fragment)
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 31 Mar 1992 #sequence_revision 31 Mar 1992 #ext_change 16-Jul 1999
 C/Accession: JH0476; S29072
 R/Schmidt, M.; Sharma, H.S.; Scholtz, R.J.; Schaper, W.
 Biochem. Biophys. Res. Commun. 180, 853-859, 1991
 A/Title: Amplification and sequencing of mRNA encoding acidic fibroblast growth factor
 A/Reference number: JH0476; M010:92062117
 A/Accession: JH0476
 A/Molecule type: mRNA
 A/Residues: 1-152 (SCH)
 A/Cross-references: EMBL:X68317; NID:91873; PIDN:CAA2869.1; FID:91874
 A/Experimental source: heart
 A/Note: the hydrophobic core residues are packed around the internal symmetry axis
 C/Comment: this protein belongs to the fibroblast growth factor family.
 C/Superfamily: fibroblast growth factor
 C/Keywords: growth factor; heparin binding
 F13/Binding site: heparin (lys) #status predicted

Query Match

22.88; Score 255; DB 2; Length 152;

Best Local Similarity 36.68; Pred. No. 1-30-16;
 Matches 63; Conservative 22; Mismatches 51; Indels 46; Gaps 4;

QY 25 FLTPVACPEPPLIGPPPSAEPSSAPWQPMAMLIHIGILRRKGLYKPTGFH-IGLLPAG 83
 DB 16 FNLDPGNPKKPKL-----LYSGNGHFLRLPAG 44
 QY 64 SVGCTTCGACACCTCTCTSVAVGLVGVGVGSLTQGMKPKPTVQSEKLTSPQLEPQF 143
 DB 45 TVDITKRSDDHQLQLSASVGEVYIKETLQVTLAMQLDGLDGLSGLPTECLLELRL 104
 QY 144 ELAWKELVAGNLYEELTCTEETVA:RLEETTPPEVAFEPSEKPTHTLPQV 195
 DB 105 EENHNYIVLSK-KMAD-KMFWGLKKNKSKKCHFLHVDQNALITCTLEVSID 152

RESULT 31

Query Match 22.88; Score 254; DB 2; Length 152;
 Best Local Similarity 43.98; Pred. No. 1-40-16;
 Matches 57; Conservative 22; Mismatches 47; Indels 5; Gaps 4;
 QY 59 LYGTGPH-LQLPDSVQGTROHSLFGLLETSVAVGLVGVGVGSLTQGMKPKPTVQSEKLTSPQLEPQF 127
 DB 29 LYSGNGHFLRLPAGVQKTPDSVQGTROHSLFGLLETSVAVGLVGVGVGSLTQGMKPKPTVQSEKLTSPQLEPQF 88
 QY 128 VGSGLKSLDGLTLEKGLTLMVNTVSGNLYKELTGRETVAKRGLTTRKDAKSK 167
 DB 89 VGSGLKSLDGLTLEKGLTLMVNTVSGNLYKELTGRETVAKRGLTTRKDAKSK 144
 QY 188 TRKVTPLAR 198
 DB 145 TRKVTPLAR 155

A:Map position: 4q25-4q27

A:Start codon: CTG

C:Superfamily: fibroblast growth factor

C:Keywords: alternative initiator; angiogenesis; growth factor; heparin binding; mitogen F1-210/produced basic fibroblast growth factor, 22.7K from status predicted (MAY 1982-86/origin: heparin binding status predicted F171-174/origin: heparin binding status predicted)

Query Match 19.5% Score 218.5; DB 2; Length 210;
Best local similarity 33.0%; Pred. No. 4,86-12;
Matches 67; Conservation 27; Mismatches 93; Indels 27; Gaps 67

QY 8 GGLGL-----PMLQGVDSHLLPRA-GEPPILDRKSAERS-----ARG 50
DB 12 GDMAGRGKRAVERVGRGKQKOTADPRAAFARQSRPQAGIMANSLITLHALPDG 71

QY 51 GPRAGLAHHTHLLPQKLVCF-GEHGLIPQSVAGTQGHSTPQLEISAVASVS 109
DB 72 GSRAPPPGPRD--PQALYQVWTEPLPIHPSPVAVPRSPAPVPLQGVAPPPVVS 128

QY 119 IPVSECTVGMVYVTVVSPFESPTFPGQTPRMYVYVYVYVYVYVYVYVYV 169
DB 129 LKVCANRYLAMKELQCLASKVTECFEELLESNNYVSEKY TSNVVAL 182

QY 179 RPTTEFCASPRHLPTTRH 192
DB 184 KPTGYELSKICQCKALPLP 205

RESULT 48
H46289
Keratinocyte growth factor like protein, group 11 human

C:Species: Homo sapiens (man)
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #tox_change 03 May 1996
C:Accession: B46289

Ref: Kelly, M.J.; Poch, M.; Sweeney, H.N.; Rubin, J.S.; O'Brien, S.J.; Aronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 9287-9291, 1992

Att: Emergence of the keratinocyte growth factor multigene family during the great A:Reference number: A46289; M010:93028449
A:Accession: B46289
A:Status: preliminary, not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-97 (KEL)

C:Superfamily: fibroblast growth factor

Query Match 19.1% Score 214; DB 2; Length 97;
Best local similarity 42.9%; Pred. No. 4,86-14;
Matches 42; Conservation 21; Mismatches 33; Indels 2; Gaps 1

QY 98 CPTSAVAVLSIPGVSYGVNMGKGLVYSKRLSPQIPFQFERNMYVYSNYK 157
DB 1 MELPFAVAVLAKGVSEYVLAAMEGKLYAKRECHDKRLLEHRYTAAAKMT 59

QY 158 WPTGPFYVAVP-GLSTVASEKSLGTHLHLY 195
DB 61 H--PCTHIVAVGKFTIVVPTPTGTAFAPFVA 76

RESULT 49
C46289

Keratinocyte growth factor-like protein, group 111 human

C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #tox_change 03-May-1996
C:Accession: C46289
Ref: Kelly, M.J.; Poch, M.; Sweeney, H.N.; Rubin, J.S.; O'Brien, S.J.; Aronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 9287-9291, 1992

Att: Emergence of the keratinocyte growth factor multigene family during the great A:Reference number: A46289; M010:93028449
A:Accession: C46289
A:Status: preliminary, not compared with conceptual translation

A:Molecule type: tRNA
A:Residues: 1-98 (KEL)
C:Superfamily: fibroblast growth factor

Query Match 19.1% Score 214; DB 2; Length 98;
Best local similarity 42.4%; Pred. No. 66-13;
Matches 42; Conservation 22; Mismatches 32; Indels 2; Gaps 1

QY 47 LLEFSAVAVSEFSEFSEFSEFSEFSEFSEFSEFSEFSEFSEFSEFSEFSE 156
DB 1 LHEFSAVAVSEFSEFSEFSEFSEFSEFSEFSEFSEFSEFSEFSEFSEFSE 156

QY 157 KCTGCRKLVALKKGLSPFQSRKPKTHTRPV 195
DB 59 KMTNDRMVALEKFTIVVPTPTGTAFAPFVA 184

RESULT 40
A48844

Basic fibroblast growth factor - chicken

C:Species: Gallus gallus (chicken)
C:Date: 01-Dec-1993 #sequence_revision 01-Dec-1994 #tox_change 16-Jul-1999
C:Accession: A48844; S23636

Ref: Kelly, A.S.; Mollnes, S.; O'Brien, R.
Dev. Biol. 157, 110-118, 1993

Att: Identification of alternative splicing of the basic fibroblast growth factor and antisense A:Reference number: A48844; M010:93426093
A:Accession: A48844
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-189 (SBR)

A:Experimental source: embryo
A:Ref: sequence obtained from cDNA library (EMBL) (1993, 2000, 2001, 2002)
R.M. Kelly, E.J. Greenbaum, Y.J. Shebat, H.J. Yip, L.
Development 109, 487-493, 1990

Att: Fibroblast growth factor during mesoderm induction in the early chick emb A:Reference number: S23636; M010:9092254
A:Accession: S23636
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 95-128 (MT)

A:Cross references: EMBL: X6664; M010:9346556; EMBL: X6664; M010:9346556
C:Superfamily: fibroblast growth factor

Query Match 18.9% Score 211.5; DB 2; Length 189;
Best local similarity 33.7%; Pred. No. 1,96-12;
Matches 45; Conservation 24; Mismatches 81; Indels 24; Gaps 67

QY 14 CPTSAVAVLSIPGVSYGVNMGKGLVYSKRLSPQIPFQFERNMYVYSNYK 157
DB 1 MELPFAVAVLAKGVSEYVLAAMEGKLYAKRECHDKRLLEHRYTAAAKMT 59

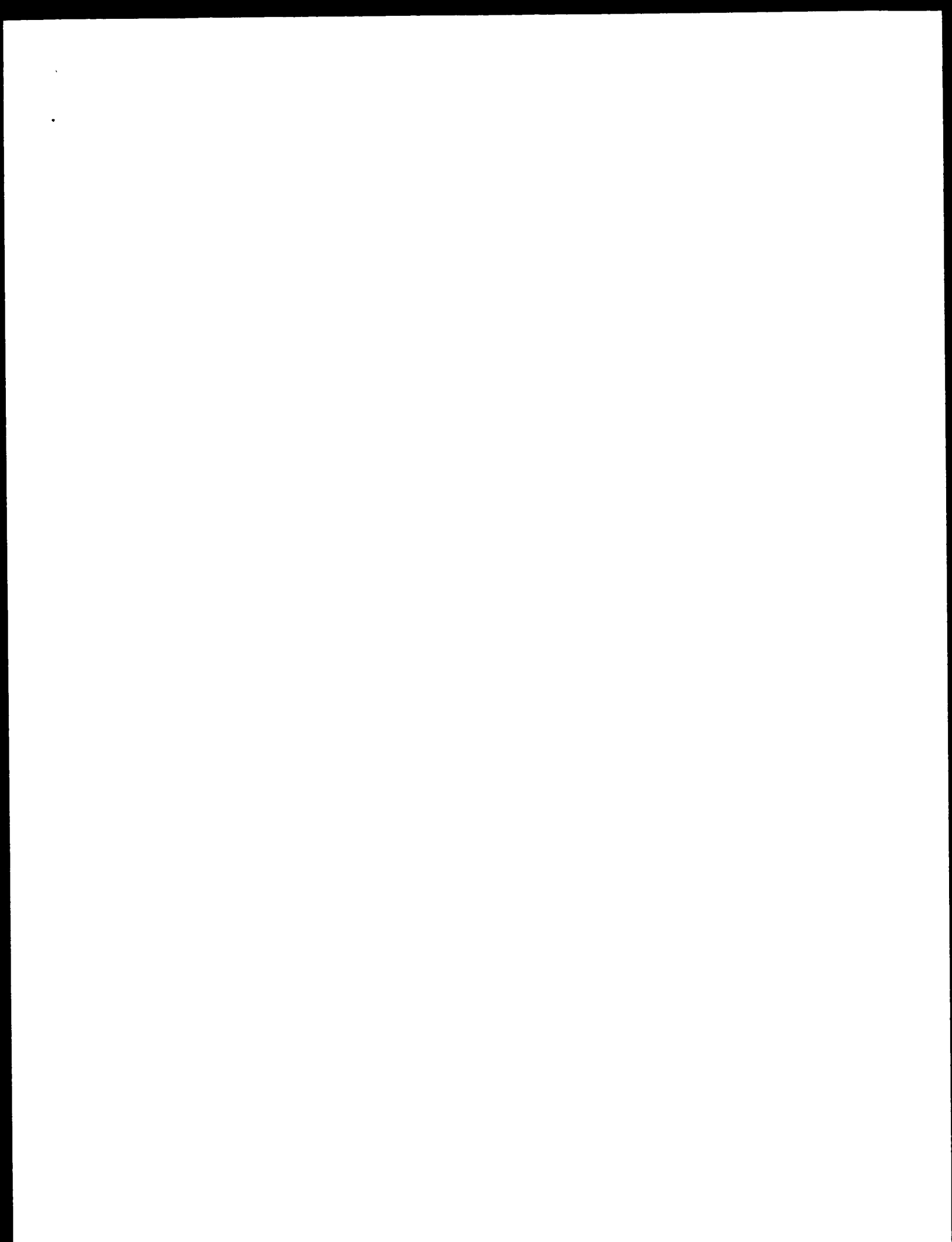
QY 158 WPTGPFYVAVP-GLSTVASEKSLGTHLHLY 195
DB 1 MELPFAVAVLAKGVSEYVLAAMEGKLYAKRECHDKRLLEHRYTAAAKMT 59

QY 160 KSKKDKGKTHTRPV 192
DB 172 KPTGYELSKICQCKALPLP 205

RESULT 41
GK608

Basic fibroblast growth factor precursor - bovine (fragment)

N:Alternative names: bFGF; kidney-derived growth factor; pro-α1(III)
C:Species: Bos taurus (cattle)
C:Date: 12-Jun-1988 #sequence_revision 02-Jul-1997 #tox_change 24-Nov-1999



EX STAIN FVB;
 RX MEDLINE: 96139512; PubMed: 9576175;
 RA Santos-Ocampo S., Colvin J.S., Chelliah A.L., Coniz D.M.;
 RT "Expression and biological activity of mouse fibroblast growth
 KT factor-9.";
 KL J. Biol. Chem. 271:1726-1731(1996).
 LN [2]
 PP SEQUENCE FROM N.A.
 RX MEDLINE: 95385801; PubMed: 7656983;
 FA S. M. Y. Li et al.
 RT "Retinoic acid induces gene expression of fibroblast growth factor 9
 KT during induction of neuronal differentiation of mouse embryonal
 RI carcinoma F9 cells.";
 RL FEBS Lett. 370:271-276(1995).
 LN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96192599; PubMed: 8619928;
 RA Hecht D., Zimmerman N., Bedford M., Avivi A., Yayon A.;
 RT "Identification of fibroblast growth factor 9 (FGF9) as a high
 KT affinity, heparin dependent ligand for FGF receptors 3 and 2 but not
 RL for FGF receptors 1 and 4.";
 LN Growth Factors 12:223-233(1995).
 KP [4]
 RP SEQUENCE FROM N.A.
 KC STRAIN 129/SVJ;
 KA Colvin J.S., Feldman B., Nadeau J.H., Goldfarb M., Coniz D.M.;
 RT Colvin J.S., Feldman B., Nadeau J.H., Goldfarb M., Coniz D.M.;
 KT "Genetic organization and embryonic expression of the mouse fibroblast
 growth factor 9 gene.";
 RL Submitted (Apr. 1995) to the EMBL database.
 CC CC -1- FUNCTION: MAY HAVE A ROLE IN GLIAL CELL GROWTH AND DIFFERENTIATION
 CC DURING DEVELOPMENT. GROWS DURING REPAIR AND REGENERATION OF
 CC BRAIN TISSUE AFTER DAMAGE. OVEREXPRESSION AND SURVIVAL OF
 CC NEURONAL CELLS, AND GROWTH STIMULATION OF GLIAL TUMORS.
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR FAMILY.
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/unimucy/>
 CC or send an email to lisb@isb.ch).
 CC
 DR EMBL: D43535; AA552529.1; -;
 DR EMBL: D48258; BA007410.1; -;
 DR EMBL: S83023; AA36429.1; -;
 DR EMBL: AF144526; AA39222.1; -;
 DR EMBL: AF144524; AA39222.1; -;
 DR EMBL: AF144525; AA39222.1; -;
 DR HSSP: J05239; 2XX.
 DR MDJ: M01104723; p019.
 DR InterPro: IPR002200; HGFc_HGF.
 DR InterPro: IPR002448; IL1_HGF.
 DR Pfam: PF0016; FGF_1.
 DR PRINTS: PR00262; ILHGF.
 DR PRINTS: PR00263; HSGF_HGF.
 DR ProDom: PD000831; HSGF_HGF_1.
 DR SMART: SM00437; p027_1.
 DR PROSITE: PS00247; HGFc_FGF_1.
 KW Growth factor; differentiation; Mitogen; Heparin-binding;
 KW Glycoprotein.
 FT PROPEP 1 3 BY SIMILARITY.
 FT CHAIN 79 208 GLIA-ACTIVATING FACTOR.
 FT CARBOHYD 79 79 N-LINKED (GLYCANIC) (POTENTIAL).
 SE SPOTLIGHT 208 AA: 23440 MW: 26000
 SE EMBL: D43535, D48258, S83023, AF144526, AF144524, AF144525, J05239, M01104723, M01104724, M01104725, M01104726, M01104727, M01104728, M01104729, M01104730, M01104731, M01104732, M01104733, M01104734, M01104735, M01104736, M01104737, M01104738, M01104739, M01104740, M01104741, M01104742, M01104743, M01104744, M01104745, M01104746, M01104747, M01104748, M01104749, M01104750, M01104751, M01104752, M01104753, M01104754, M01104755, M01104756, M01104757, M01104758, M01104759, M01104760, M01104761, M01104762, M01104763, M01104764, M01104765, M01104766, M01104767, M01104768, M01104769, M01104770, M01104771, M01104772, M01104773, M01104774, M01104775, M01104776, M01104777, M01104778, M01104779, M01104780, M01104781, M01104782, M01104783, M01104784, M01104785, M01104786, M01104787, M01104788, M01104789, M01104790, M01104791, M01104792, M01104793, M01104794, M01104795, M01104796, M01104797, M01104798, M01104799, M01104800, M01104801, M01104802, M01104803, M01104804, M01104805, M01104806, M01104807, M01104808, M01104809, M01104810, M01104811, M01104812, M01104813, M01104814, M01104815, M01104816, M01104817, M01104818, M01104819, M01104820, M01104821, M01104822, M01104823, M01104824, M01104825, M01104826, M01104827, M01104828, M01104829, M01104830, M01104831, M01104832, M01104833, M01104834, M01104835, M01104836, M01104837, M01104838, M01104839, M01104840, M01104841, M01104842, M01104843, M01104844, M01104845, M01104846, M01104847, M01104848, M01104849, M01104850, M01104851, M01104852, M01104853, M01104854, M01104855, M01104856, M01104857, M01104858, M01104859, M01104860, M01104861, M01104862, M01104863, M01104864, M01104865, M01104866, M01104867, M01104868, M01104869, M01104870, M01104871, M01104872, M01104873, M01104874, M01104875, M01104876, M01104877, M01104878, M01104879, M01104880, M01104881, M01104882, M01104883, M01104884, M01104885, M01104886, M01104887, M01104888, M01104889, M01104890, M01104891, M01104892, M01104893, M01104894, M01104895, M01104896, M01104897, M01104898, M01104899, M01104900, M01104901, M01104902, M01104903, M01104904, M01104905, M01104906, M01104907, M01104908, M01104909, M01104910, M01104911, M01104912, M01104913, M01104914, M01104915, M01104916, M01104917, M01104918, M01104919, M01104920, M01104921, M01104922, M01104923, M01104924, M01104925, M01104926, M01104927, M01104928, M01104929, M01104930, M01104931, M01104932, M01104933, M01104934, M01104935, M01104936, M01104937, M01104938, M01104939, M01104940, M01104941, M01104942, M01104943, M01104944, M01104945, M01104946, M01104947, M01104948, M01104949, M01104950, M01104951, M01104952, M01104953, M01104954, M01104955, M01104956, M01104957, M01104958, M01104959, M01104960, M01104961, M01104962, M01104963, M01104964, M01104965, M01104966, M01104967, M01104968, M01104969, M01104970, M01104971, M01104972, M01104973, M01104974, M01104975, M01104976, M01104977, M01104978, M01104979, M01104980, M01104981, M01104982, M01104983, M01104984, M0110

1	MAPLEVEGETATION.PLOT.GROWTH.SHEET1.PLOT.DEPH.DT.CPP.SPAN.ABS.PLOT----	10/1/2000	67
QY			
	Quarterly Match Similarity	69.34%	Score 774.57
	Prod. Local Similarity	70.64%	Prod. 774.34
	Matches	149	Conservation
		22	Mismatches
		30	Inserts
		9	Deletes
		4	

[illegible]

	GLYCOPROTEIN	RY SIMILARITY
KW	1	2
ET	1	2
ET	202	202
CHARN	79	79
CARBOND	238	238
ET	79	79
SID	23414	23414
SEQUENCE	400	400

DE FEM3; D64085; HAA10966; 1; -;
DE FEM3; D64086; HAA10967; 1; -;
DE HSS3; P00038; 1B5⁺;
DE Int 6770; PR002209; HBGF; FGF;
DE Int 6770; PR002348; 1L1 HBGF;
DE P1am; PR00167; FGF; 1.

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FT	DOMAIN	53	59	POLY-SER.
FT	CARBOHYD	106	108	N-TERMIN (SEQUENCE) (CONTINUED)
FT	VARSPPLIC	118	121	LEFT (GIVE IN SHORT ISOFORM)
FT	VARSPPLIC	122	264	MISSING (IN SHORT ISOFORM)
50	SYNTHETIC	264 AA	264 AA	FRAGMENTED (IN SHORT ISOFORM)

Query Match	28.7%	Score 321	DB 1	Length 264
Best Local Similarity	40.3%	Freq. Nov. 9 to 23		
Matches	84	Conservative 22	Mismatches 75	Indels 25
				GCAT 7

[illegible]

RESULT	14
FGF3_HUMAN	
ID	FGF3_HUMAN
STANDARD;	
PRT;	239 AA

DT	01-OCT-1989 (Rel. 12, created)
DT	01-OCT-1989 (Rel. 12, last sec)

DE INT 2 PHOSPHONOSULFONIC ACID (FIBROBLAST OR WITH FACTOR 3),
DE INT 4 (HMG 3),
DE (FGE 4) OR INT2
CN FGE4 OR INT2

05 Homo sapiens (human);
06 Eukaryota; Metazoa; Chordata; Vertebrata; Molluscophora;
07 Mammalia; Eulipotyphla; Primates; Carnivora; Hominoidea; Homo.

RN 11
RP SEQUENCE FROM N.A.

RX MEDLINE-89239468; PubMed 2470007;
RA Provasi S Smith S Casey G Thompson J
Provasi S Smith S Casey G Thompson J

CC -1- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT

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DR EMILIO M14457 CAA32615.117
DR PIR: S04742; S04742.
DR HSSP: p09038; 2BFH.

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DR      InterPro: IPR002209;  HMMF_EGF
DR      InterPro: IPR002348;  H1_HHGF.
DR

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DR PRINTS: PRO0262; 111HR07.
DR PRINTS: PRO0263; HBGF05F.

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DR SMART; SMO0442; FGF; 1.
DR PROSITE; PS00247; HMGF_FGF; 1.
```

	Transforming Protein: Oncogene	Growth Factor	Mitogen	Signal
KW	glycoprotein			
6M	1	17	18	19
IT	20	21	22	23
ET	24	25	26	27
IT	28	29	30	31
IT	32	33	34	35
IT	36	37	38	39
IT	40	41	42	43
IT	44	45	46	47
IT	48	49	50	51
IT	52	53	54	55
IT	56	57	58	59
IT	60	61	62	63
IT	64	65	66	67
IT	68	69	70	71
IT	72	73	74	75
IT	76	77	78	79
IT	80	81	82	83
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Only Match Simulated	28.7%	29.0%	29.3%	29.5%	29.7%	29.9%	30.1%	30.3%	30.5%	30.7%	30.9%	31.1%	31.3%	31.5%	31.7%	31.9%	32.1%	32.3%	32.5%	32.7%	32.9%	33.1%	33.3%	33.5%	33.7%	33.9%	34.1%	34.3%	34.5%	34.7%	34.9%	35.1%	35.3%	35.5%	35.7%	35.9%	36.1%	36.3%	36.5%	36.7%	36.9%	37.1%	37.3%	37.5%	37.7%	37.9%	38.1%	38.3%	38.5%	38.7%	38.9%	39.1%	39.3%	39.5%	39.7%	39.9%	40.1%	40.3%	40.5%	40.7%	40.9%	41.1%	41.3%	41.5%	41.7%	41.9%	42.1%	42.3%	42.5%	42.7%	42.9%	43.1%	43.3%	43.5%	43.7%	43.9%	44.1%	44.3%	44.5%	44.7%	44.9%	45.1%	45.3%	45.5%	45.7%	45.9%	46.1%	46.3%	46.5%	46.7%	46.9%	47.1%	47.3%	47.5%	47.7%	47.9%	48.1%	48.3%	48.5%	48.7%	48.9%	49.1%	49.3%	49.5%	49.7%	49.9%	50.1%	50.3%	50.5%	50.7%	50.9%	51.1%	51.3%	51.5%	51.7%	51.9%	52.1%	52.3%	52.5%	52.7%	52.9%	53.1%	53.3%	53.5%	53.7%	53.9%	54.1%	54.3%	54.5%	54.7%	54.9%	55.1%	55.3%	55.5%	55.7%	55.9%	56.1%	56.3%	56.5%	56.7%	56.9%	57.1%	57.3%	57.5%	57.7%	57.9%	58.1%	58.3%	58.5%	58.7%	58.9%	59.1%	59.3%	59.5%	59.7%	59.9%	60.1%	60.3%	60.5%	60.7%	60.9%	61.1%	61.3%	61.5%	61.7%	61.9%	62.1%	62.3%	62.5%	62.7%	62.9%	63.1%	63.3%	63.5%	63.7%	63.9%	64.1%	64.3%	64.5%	64.7%	64.9%	65.1%	65.3%	65.5%	65.7%	65.9%	66.1%	66.3%	66.5%	66.7%	66.9%	67.1%	67.3%	67.5%	67.7%	67.9%	68.1%	68.3%	68.5%	68.7%	68.9%	69.1%	69.3%	69.5%	69.7%	69.9%	70.1%	70.3%	70.5%	70.7%	70.9%	71.1%	71.3%	71.5%	71.7%	71.9%	72.1%	72.3%	72.5%	72.7%	72.9%	73.1%	73.3%	73.5%	73.7%	73.9%	74.1%	74.3%	74.5%	74.7%	74.9%	75.1%	75.3%	75.5%	75.7%	75.9%	76.1%	76.3%	76.5%	76.7%	76.9%	77.1%	77.3%	77.5%	77.7%	77.9%	78.1%	78.3%	78.5%	78.7%	78.9%	79.1%	79.3%	79.5%	79.7%	79.9%	80.1%	80.3%	80.5%	80.7%	80.9%	81.1%	81.3%	81.5%	81.7%	81.9%	82.1%	82.3%	82.5%	82.7%	82.9%	83.1%	83.3%	83.5%	83.7%	83.9%	84.1%	84.3%	84.5%	84.7%	84.9%	85.1%	85.3%	85.5%	85.7%	85.9%	86.1%	86.3%	86.5%	86.7%	86.9%	87.1%	87.3%	87.5%	87.7%	87.9%	88.1%	88.3%	88.5%	88.7%	88.9%	89.1%	89.3%	89.5%	89.7%	89.9%	90.1%	90.3%	90.5%	90.7%	90.9%	91.1%	91.3%	91.5%	91.7%	91.9%	92.1%	92.3%	92.5%	92.7%	92.9%	93.1%	93.3%	93.5%	93.7%	93.9%	94.1%	94.3%	94.5%	94.7%	94.9%	95.1%	95.3%	95.5%	95.7%	95.9%	96.1%	96.3%	96.5%	96.7%	96.9%	97.1%	97.3%	97.5%	97.7%	97.9%	98.1%	98.3%	98.5%	98.7%	98.9%	99.1%	99.3%	99.5%	99.7%	99.9%
Best Match Simulated	10.0%	10.1%	10.2%	10.3%	10.4%	10.5%	10.6%	10.7%	10.8%	10.9%	11.0%	11.1%	11.2%	11.3%	11.4%	11.5%	11.6%	11.7%	11.8%	11.9%	12.0%	12.1%	12.2%	12.3%	12.4%	12.5%	12.6%	12.7%	12.8%	12.9%	13.0%	13.1%	13.2%	13.3%	13.4%	13.5%	13.6%	13.7%	13.8%	13.9%	14.0%	14.1%	14.2%	14.3%	14.4%	14.5%	14.6%	14.7%	14.8%	14.9%	1																																																																																																																																																																																																																																																																																																																	

17 PAAGDAH.....HFA.....HDA.....YHHTAAPEPELYATKXHLGLHPSTVWG 66

D0 67 S-LENSAVALIETIAVIOVAIKOLISUAMAKROINTYASINHYSALEHVEITHHO 12

DY 148 INTENSIVY KHOTJENIVALNIEZHREKASNOBUEFTIHLEPVIDP 19

QY 198 ERPEL,YKDL, 207
1 | : : 1

RESULT 15
FOR_MOUSE

DT	01-NOV-1988	(Rel. 09, Created)
DT	01-NOV-1988	(Rel. 09, Last sequence update)
DT	01-NOV-1995	(Rel. 32, Last annotation update)

GN FGF3 OR FGF3-3 OR INT-2,
00 Mus musculus (Mouse),
00 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RN	11
RP	SEQUENCE FROM N.A.
RX	MEDLINE=8624750Z; PUBMED 3013624;

RT protective efficacy of inactivated by mouse mammary tumour virus." *J.*
 RL *EMBO J.*, 5: 919-924 (1986).
 RN [2]

PA Smith E., Roberts G., Jackson C.J.
PT "Multiple RNAs expressed from the int-2 gene in mouse embryonal
FI carcinoma cell lines encode a protein with homology to fibroblast

EN	[3]
RP	CHARACTERIZATION.
RX	MEULINF=91193291; PubMed=1964688;

RI "Characterization of int-2: a member of the fibroblast growth factor family."
 RI
 EL J. Cell Sci. Suppl. 13:87-96 (1990).

CC -I- SIMILARITY: BELONGS TO THE HEPATIN-BINDING GROWTH FACTORS FAMILY
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its

RL The fibroblast growth factor family.*
 RL Biol. Chem. 271:15918-15921(1996).
 CC FUNCTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WOUND
 CC HEALING. ACTS AS A MITOGEN IN THE JOINT. MAY ACT IN A MAJORITY
 CC SIMILAR TO FGF-7.
 CC SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
 CC TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE LUNG IN
 CC ADULTS.
 CC SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC
 DR EMBL: D07921; GenBank: U01146.1;
 DR InterPro: IPR002209; HMGF_FGF.
 DR InterPro: IPR002448; H1_HMGF.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR002462; H1HMGF.
 DR PROSITE: PS00247; HMGF_FGF; 1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HMGF_FGF; 1.
 DR Growth factor: Glycoprotein. Signal.
 DR SIGNAL: 1 46 POTENTIAL.
 DR CHAIN: 47 215 FIBROBLAST GROWTH FACTOR-10.
 DR DOMAIN: 51 69 POLY-SER.
 DR CATHEDRAL: 50 50 N-LINKED (GLYCNA:...) (POTENTIAL).
 DR CATHEDRAL: 204 204 N-LINKED (GLYCNA:...) (POTENTIAL).
 DR SOURCE: 215 AA; 24029 MW; 947786FA6FC0866A CRC64;
 SO
 Query Match 27.5% Score 368, DB 1, Length 215,
 Best Local Similarity 36.4% Pred. No. 1, 1e-21;
 Matches 66, Conservative 43, Mismatches 67, Indels 10, Gaps 3.
 QY 19 GAVAGVHLLDVAHRTVLLTTPSSVAHSAKAPGMA GAHHPHIFPFGVYCN 73
 DB 47 GAVAGVHLLDVAHRTVLLTTPSSVAHSAKAPGMA GAHHPHIFPFGVYCN 73
 QY 74 GPHLLTPHPSVQGRKQHSLLPFLTSAVAVIVSLKGVSDVLAAMKNCALYSEKL 133
 DB 74 GPHLLTPHPSVQGRKQHSLLPFLTSAVAVIVSLKGVSDVLAAMKNCALYSEKL 133
 QY 94 FTLKLTPEKVSCTKFTFVCTTCTCVFVVAVVAFVHSNYVAMKCKELYSCKET 159
 DB 94 FTLKLTPEKVSCTKFTFVCTTCTCVFVVAVVAFVHSNYVAMKCKELYSCKET 159
 QY 144 TTECTVDSGLDHWTVYSNLYHSGTGGPVVALNKGTPVCAAPVHCKFTHEHP 194
 DB 144 TTECTVDSGLDHWTVYSNLYHSGTGGPVVALNKGTPVCAAPVHCKFTHEHP 194
 QY 194 PV 196
 DB 212 VV 214
 RESULT 20
 FROM HUMAN
 ID FROM HUMAN STANDARD: PRT: 170 AA.
 AC G96F02
 DT 20 AUG 2001 (rel. 40, last sequence update)
 DT 20 AUG 2001 (rel. 40, last annotation update)
 DE FIBROBLAST GROWTH FACTOR-22 PRECURSOR (FGF-22).
 GN FGF22.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID:9606;
 RN 111
 RP SEQUENCE FROM N.A.
 RC TISSUE: Placenta;

RX MEDLINE:21240339; PubMed:11342227;
 RA Nakatani Y., Hoshikawa M., Asaki T., Kassai Y., Itoh N.,
 RT Identification of a novel fibroblast growth factor, FGF 22,
 RT preferentially expressed in the inner root sheath of the hair
 RT follicle.*
 RT Biochim. Biophys. Acta 1517:460-463(2001).
 CC FUNCTION: MAY BE INVOLVED IN HAIR DEVELOPMENT.
 CC SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
 CC SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 CC
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 CC
 DR EMBL: AB021925; BAB14479.1;
 DR MIM: 605831;
 DR InterPro: IPR002209; HMGF_FGF.
 DR InterPro: IPR002448; H1_HMGF.
 DR Pfam: PF00167; FGF_1.
 DR PROSITE: PS00247; HMGF_FGF; 1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HMGF_FGF; FALSE_NEG.
 DR Growth factor: Signal.
 DR SIGNAL: 1 22 POTENTIAL.
 DR CHAIN: 23 170 FIBROBLAST GROWTH FACTOR-22.
 DR SOURCE: 170 AA; 19662 MW; C88891BC215AC67 CRC64;
 SO
 Query Match 27.5% Score 307, DB 1, Length 170,
 Best Local Similarity 45.0% Pred. No. 1, 1e-21;
 Matches 66, Conservative 23, Mismatches 56, Indels 4, Gaps 2;
 QY 42 SAAPSPAPGPGACAI AHI HGII PRPOLYCRGFGHIIIPROSVGSTRQDHSIFGLIEFI 101
 DB 42 SAAPSPAPGPGACAI AHI HGII PRPOLYCRGFGHIIIPROSVGSTRQDHSIFGLIEFI 101
 QY 20 AATSPASAPF--PSYHLEFGVWPMPLESTHEFI PVDPGVVGTTRKMRHSDSTLEIR 77
 DB 20 AATSPASAPF--PSYHLEFGVWPMPLESTHEFI PVDPGVVGTTRKMRHSDSTLEIR 77
 QY 102 SVAAGVSVTPGVDSGLYGLNCKGPGFYASRKTSPQTPFQPEPNMYNYSNRYKQDI 161
 DB 78 SVAAGVSVTPGVDSGLYGLNCKGPGFYASRKTSPQTPFQPEPNMYNYSNRYKQDI 161
 QY 162 GPEYVALNFGVTPPVAVSPYRQKFTHEHP 192
 DB 136 GQPMPLAIDPRGSPRPGSKTRVHLSAHELP 166
 RESULT 21
 FROM HUMAN
 ID FROM HUMAN STANDARD: PRT: 256 AA.
 AC P48802;
 DT 01-FEB-1996 (rel. 33, last sequence update)
 DT 01-FEB-1996 (rel. 33, last annotation update)
 DE FIBROBLAST GROWTH FACTOR-3 PRECURSOR (FGF-3) (HMGF-3).
 GN FGF3 OR FGF-3.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Danio; Danio; Danio.
 CC Cypriniformes; Cyprinidae; Rasbora; Rasbora.
 CC NCBI_TaxID:7956;
 RN 111
 RP SEQUENCE FROM N.A.
 RA MEDLINE:96204005; PubMed:8622866;
 RA Kiefer P., Strahle U., Mason I., Dieckson C.,
 RT Secretion and mitogenic activity of zebrafish FGF3 reveal
 RT intermediate properties relative to mouse and Xenopus homologues.*
 RT Oncogene 12:1503-1511(1996).
 CC -1- FUNCTION: POTENT MITOGEN AND TRANSPORTING AGENT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.


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000 Enkaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
001 Mammalia; Eutheria; Rodentia; Sciurumorphi; Muridae; Murinae; Mus;
002 NCBI_Taxid:10090;
003
004
005 SEQUENCE FROM N.A.
006 MEDLINE:97473538; PubMed:9332392;
007 RA Tagashira S., Harada H., Katsumata T., Itoh N., Nakatsuka M.;
008 "Cloning of mouse FGF10 and up-regulation of its gene expression
009 during wound healing.";
010 Gene 197;399-404(1997);
011
012
013 SEQUENCE FROM N.A.
014
015 TISSUE:Lung;
016
017 Duan D.R., Florence C.;
018 Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
019
020 FUNCTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WOUND
021 HEALING. ACTS AS A MITOGEN IN THE LUNG. MAY ACT IN A HAPHER
022 SIMILAR TO FGF-7.
023
024 -1- SINGLE CELLULAR LOCATION: SECRETED (POTENTIAL).
025
026 -1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN EMBRYOS AND THE LUNG,
027 AND AT MUCH LOWER LEVELS IN HEART AND HEART.
028
029 -1- SIMILARITY: BELONGS TO THE HEPARIN BINDING GROWTH FACTORS FAMILY.
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039
040
041 EMBL: D89480; BAA22836.1; -;
042 DR EMBL: U94517; A0000761.1; -;
043 DR MGD: MGI:1099809; FGF10.
044
045 InterPro: IPR002209; HGFG_FGF.
046
047 InterPro: IPR002348; I11_HBGF.
048
049 Pfam: PF00167; FGF; 1.
050
051 DR PRINTS: PR00262; I11HBGF.
052 DR PRINTS: PR00263; HBGFEGF.
053 DR TrEMBL: F103083; HBGF_FGF; 1.
054
055 SMART: SM03432; FGF; 1.
056
057 PROSITE: PS00247; HBGF_FGF; 1.
058
059 Growth factor, glycoprotein; Signal.
060
061 FT SIGNAL 1 36
062 FT CHAIN 37 209
063 FT DOMAIN 52 63
064 FT CARBOHYD 50 50
065 FT CARBOHYD 197 197
066
067 SEQUENCE 209 AA; 23597 MW; 7FD2227844343CC GRG4;
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RI Proc. Natl. Acad. Sci. U.S.A. 93:9850-9857 (1996)
CC - FUNCTION: PROBABLY INVOLVED IN NERVOUS SYSTEM DEVELOPMENT AND
CC FUNCTION.
CC - TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC - SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC at Hinxton Road, Cambridge CB2 0AT, UK.
DR PMID: 861199; AARI8945.1;
DR HSSB: P05320; BAXM.
DR MIM: 601514;
DR InterPro: IPR002209; HBGF_FGF
DR Pfam: PF00167; FGF_1
DR ProDom: PD000831; HBGF_FGF_1
DR SMART: SM00442; FGF_1
DR PfamSF: SF00247; HBGF_FGF_1
KW Growth factor;
SQ Shegkhpv_25 AA: 25305 MW: 41274.205 kDa 220 COPS 1;
Query Match: 24 9% Score 378.5 DB 1 Length 225;
Best local similarity: 35 7% E=0.00000E+00
Matches: 66 Conservative: 28 Mismatches: 67 Indels: 25 Gaps: 4;
QY 24 PATSEPP-----IIEPVSAPEVAGCPMAVAHLEILRR 67
DB 18 PAISPEVASGKRVCHGKSLQNGDITLSVPLDGSHAV--PDSHPGLKIVLR 74
QY 64 QIVCTGPGQLTIIPGVSVTHPGWSTPIHLIFTSAAVGI VSLPVDNLTLCMKPKEL 127
DB 76 LEPCECVLDMNPSPSIQTPETYSPTPHRPLVLELVTVLSAFTSYNAKMAEDLL 173
QY 138 YGGRTTGTATPEPFEEEMNTVEENIVEDETCHEFVALIKQTHIDAFREGRHCF 187
DB 144 YSSPTATCLDFHHVLEMLVYLVSALAEHSASAWLDLDDGYMKZNRVKIKFAA 193
QY 188 THFLRP 193
DB 194 AHFLPK 199
RESULT 37
L756_CAHEL
ID L756_CAHEL STANDARD: PPT: 413 AA
AC Q11184;
DT 01-NOV-1997 (rel 35, created)
DI 01-NOV-1997 (rel 35, last sequence update)
DI 15-JUL-1998 (rel 36, last annotation update)
DE LET-756 PROTEIN.
GN LET-756 OR COSD11.4.
OS Caenorhabditis elegans.
OC Eukaryota, Metazoa, Nematoa, Chromadorea, Rhabditida, Nematoda.
OC Pholidipoda, Polychordata, Cephalochordata.
OX NCBI_TaxId=6219;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RL Du Z...
CC - SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC      or send an email to license@sb-sib.ch)
CC      EMIL: 009048; AAB54825-1; -
DR      HSSB; P06570; 2AXM.
DR      WormPep; C05011_4; GE01114.
DR      InterPro; IPRO02209; HMGE_FGF.
DR      Pfam; PF0167; FGF_1.
DR      ProDom; PD000831; HMGE_FGF_1.
DR      SMART; SMC0442; FGF_1.
DR      Pfam; PF0247; HMGE_FGF_1.
SV      SEQUENCE: 413 AA, 46116 MW, 7667022AAV05BAC_CRYG4;

Query Match:
Post Local Similarity: 42.98; Score: 278; DR: 1; Length: 413;
Matches: 67; Consistency: 67; Missed: 54; Models: 20; Gaps: 57

CC      40 PSSAEPASAPDQPSVALAHMLHLLHPALVCFYCEHLQIDP-----DSN---VQTRQ 90
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      PROLDREDFNYTHAD-----PPRALHPSPWLMFLPIFDNDSPSTVVAVCHKE 106
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC      91 ESHLFTTLLTSANCLSTVGVSTSLTGLKATPTLV--SPETSPSTTPPLPVFNKY 148
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC      107 ESSEKIVAFVSVAALVAFQVVERKNLDMPSRVLATESYSTVELEEMENY 166
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC      149 RYSSTVFHTCTEFVALFEECTECGAFPRNGRTGRPFVTFVTV 200
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC      151 LLSVALI DLTMDLLHSLSLRDRAAGFFRSASHLYVHHLDLI 216
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 48
FCRM_MOUSE STANDARD PRS: 2.5 AA.
P70378:
DE      01 NOV-1997 (rel. 45, created)
DT      01 NOV-1997 (rel. 45, last sequence update)
DI      1 N.Y. 1997 (rel. 45, last annotation update)
DE      FIBROBLAST GROWTH FACTOR-11 (FGF-11) (Fibroblast Growth Factor
DR      HOMOLOGOUS FACTOR 3) (PHF-3).
CN      FGFI1 OR PHF3.
OS      Mus musculus (Mouse).
OC      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Ox      Mammalia; Eutheria; Rodentia; Sciurimorphi; Muridae; Murinae; Mus.
RN      NCBI TaxId=10090;
RP      111
RV      SEQUENCE FROM N.A.
RX      TISSUE-EYE;
RX      MEDLINE 96382556; PubMed 8790420;
PA      Smallwood F.M., House J.D., Jia T., Lee P., Mahe J.P., Nathans J.;
EA      "Fibroblast growth factor (FGF) homologous factors: new members of
FT      the FGF family implicated in nervous system development.";
EL      Proc. Natl. Acad. Sci. U.S.A. 93:9656-9657(1996);
CC      1 FUNCTION: PROBABLY INVOLVED IN NERVOUS SYSTEM DEVELOPMENT AND
       FUNCTION.
CC      -1 SUBCELLULAR LOCATION: NONEAR (PROBABLY).
CC      1 TISSUE SPECIFICITY: BRAIN AND EYE, AND IN A CHARACTERISTIC PATTERN OF
       THE EMBRYONIC BODY WALL. IS ABSENT EXACTLY BY EYE, RETICULUM AND
CC      MOST CONCENTRATED IN PURKINE CELL LAYER OF THE CEREBELLUM.
CC      -1 SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC      -----
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CC      entities requires a license agreement with the provider of the service or
CC      or send an email to license@sb-sib.ch).
CC      PMID: 066203; AAB18919.1; -
DR      HSSB; P04968; IBAE.
DR      MPI; MGI-109167; Fgf11.

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DR InterPro: IPR002209; HGFP_FGF.
 DR Pfam: PF00167; FGF_1.
 DR ProDom: PD000831; HGFP_FGF_1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HGFP_FGF_1
 KW Growth factor.
 SQ SEQUENCE: 225 AA; 25179 MW; 11343499561441 CP664;

Query Match: 24.4%; Score 271.5; DB 1; Length 225;
 Best Local Similarity: 44.2%; Pred. No. 36-18;
 Matches: 68; Conservative: 30; Mismatches: 74; Indels: 27; Gaps: 4;

QY 29 PAPERPP.....LIGRRSAERSAKGGAGNOLAHGILRRK 67
 ID 18 EGGSPVSAQRVPTPEKSLDQKQILLISKVLSQDPTKQDQPE POLKQIVRK 74
 QY 68 QLYTPRHQQLPKNSVQTHQDHSILGLLEFISVAVGLVSGVDSGLYGMNDKGEI 127
 ID 75 LERQCPVLCANRQSGTGTHTDPSLHFNILVTLKVVLTGSAKTHYAMNAKSL 133
 QY 128 YGSRKLTGDTLRQDILDMWTFYKRLTCEKVEVA;NELTTFEKAASKRQKE 187
 ID 144 YSSQELAVLELELVHVVLA;AVYLFEECHAVTGLIKEDYKCHPVKTKAA 193
 QY 188 HPIIRK -VYDERKVELY 204
 ID 194 AHEVRLKLVAMRPSLH 212

RESULT 49
 FGF4 HUMAN STANDARD; PRT: 206 AA.

ID FGF4_HUMAN STANDARD; PRT: 206 AA.
 AC P08020;
 DT 01 AUG 1988 (rel. 08, created)
 DT 01 AUG 1988 (rel. 08, last sequence update)
 DT 20 AUG 2001 (rel. 40, last annotation update)
 DE FIBROBLAST GROWTH FACTOR 4 PRECURSOR (FGF-4) (HEPARIN SECRETORY
 IDE TRANSFORMING PROTEIN) (HST-1) (HST) (TRANSFORMING PROTEIN KS1) (HBGF-
 ID 4)
 OS FGF4 OR HST OR HSTF OR KS1.
 OS Homo sapiens (human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OS Mammalia; Eutheria; Primates; Catartini; Homiidae; Homo.
 OX NCBI_TaxID 9606;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 88041076; PubMed 2959959;
 RA Yoshida T., Miyagawa K., Odagiri H., Sakamoto H., Little P.P.K.,
 RT Torada M., Sugimura T.;
 RT "Genomic sequence of hst, a transforming gene encoding a protein
 RT homologous to fibroblast growth factors and the int-2-encoded
 RT protein.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:7405-7409(1987).
 RN 121
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87204251; PubMed 2953041;
 RA Taira M., Yoshida T., Miyagawa K., Sakamoto H., Torada M.,
 RA Sugimura T.;
 RT "cDNA sequence of human transforming gene hst and identification of
 RT the coding sequence regulated for transforming activity.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:2980-2984(1987).
 RN 131
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 8701176; PubMed 2957062;
 RA Belli I., Curatola A.M., Korn F.G., Greco A., Ittmann M.,
 RA Bostic G.;
 RT "An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes
 RT a growth factor that is a member of the FGF family.";
 RT Cell 50:279-287(1987).
 CC FUNCTION: CAN TRANSFORM NIH 3T3 CELLS FROM A HUMAN STOMACH TUMOR
 CC (HSD) AND FROM KAPOSI'S SARCOMA (KS1). IT HAS A MITOGENIC
 CC ACTIVITY.

CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 CC
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 CC
 CC EMBL: J02986; AAB59555.1;
 CC EMBL: M17446; AAB59473.1;
 CC PIR: A28417; TVHUS.
 CC HSSP: P09038; HRF.
 CC MIM: 164980;
 CC InterPro: IPR002209; HGFP_FGF.
 CC InterPro: IPR002348; IL1_HGFP.
 CC Pfam: PF00167; FGF_1.
 CC PRINTS: PR00262; IL1HGFP.
 CC PRINTS: PR00263; HBGF_FGF.
 CC PRODOM: PD000831; HGFP_FGF_1.
 CC SMART: SM00442; FGF_1.
 CC PROSITE: PS00247; HGFP_FGF_1.
 CC TRANSFORMING PROTEIN; Oncogene; Growth factor; Mitogen; Signal.
 KW SIGNAL.
 FT CHAIN 1 27 POTENTIAL.
 FT SIGNAL 1 27 FIBROBLAST GROWTH FACTOR-4.
 SV SEQUENCE 206 AA; 22047 MW; 37ED54A0272A1569 CP664;

Query Match: 24.2%; Score 270; DB 1; Length 206;
 Best Local Similarity: 41.7%; Pred. No. 3-80-18;
 Matches: 68; Conservative: 20; Mismatches: 59; Indels: 16; Gaps: 5;

QY 33 RPLLEERSAERSARGGPMANOLAHGILRRQLYCKT--GHILQILPKNSVQSTK 90
 ID 57 RLPLVAQPKAAVQSGAD-----YLLGIKLPRIYCNVWIGPHI QALPDRIGGAA 109
 QY 91 DSHLHGLLEISAVAGVLS;P;V;LS;LI;GM;K;K;D;Y;G;E;K;L;T;S;I;F;E;C;E;N;Y;N;T 150
 ID 110 D-TRDSLESLSPERGVS;FGVASRFPVAMSSKKGLYGSPPETDTEFKHLLIPNNYNA 168
 QY 151 YSSNIYKHDIDGRFVALNKDPTPRDGAASKRHKQTHLPR 193
 ID 169 YRS-YKYPG---MFLALSKNKTKKGNVSPTMKVTHLPR 205

RESULT 40
 FGF4_BOVIN
 ID FGF4_BOVIN STANDARD; PRT: 206 AA.
 AC P48803;
 DT 01-FEB-1996 (rel. 33, created)
 DT 01-FEB-1996 (rel. 33, last sequence update)
 DT 20-AUG-2001 (rel. 40, last annotation update)
 DE FIBROBLAST GROWTH FACTOR-4 PRECURSOR (FGF-4) (HEPARIN SECRETORY
 DE TRANSFORMING PROTEIN) (HST) (HBGF-4).
 ID FGF4 OR HST.
 OS Bos taurus (bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OS Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID: 9913;
 RN 111
 RP SEQUENCE FROM N.A.
 KC TISSUE: thymus;
 RX MEDLINE: 96032369; PubMed=7557455;
 RA Yu J.-C., Desceabra A.J., Wang L.M., Fleming T.P., Chedid M.,
 RA Miki T., Heidaran M.A.;
 RT "An unexpected transforming gene in calf-thymus carrier DNA: bovine
 RT hst.";
 RT Gene 162:333-334(1995).
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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KI canine hearts";
 RI EMBL: X60317; GMA2869.1;
 CC FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANTI-GENIC AGENTS
 CC IN VIVO AND ARE PARTIAL MITOGENS FOR A VARIETY OF CELL TYPES IN
 CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC -1 SUBUNIT: MONOMER.
 CC -1 MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
 CC THAN DOES BFGF.
 CC -1 SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY
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 CC or send an email to license@ebi.ac.uk).
 CC
 DR EMBL: X60317; GMA2869.1;
 DR PIR: S0354; S0354.
 DR HSSP: P05230; ZAXM.
 DR InterPro: IPR002209; HGCF_FGF.
 DR Pfam: PF00167; FGF_1.
 DR ProDom: PD000841; HGCF_FGF_1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HGCF_FGF_1.
 KM Growth factor; Mitogen; Vascularization; Heparin-binding.
 FT PROPEP 1 15
 FT CHAIN 16 152 HEPARIN-BINDING GROWTH FACTOR 1.
 FT BINDING 22 152 ENDOTHELIAL CELL GROWTH FACTOR ALPHA.
 FT BINDING 24 28 HEPARIN (HEPENTANAL).
 FT BINDING 113 116 HEPARIN (HEPENTANAL).
 FT CONFLICT 31 31
 FT CONFLICT 39 39 R -> Y (IN REF. 2).
 FT R-TER 152 152
 SQ SEQUENCE 152 AA; 17103 MW; ABE540A92FVABF4 CMC64;
 Query Match 22.8%; Score 254.5; DB 1; Length 152;
 Best local similarity 36.6%; Pred. No. 6; Seq. 17;
 Matches 63; Conservation 23; Missions 4; Ids 14; Cops 4;
 QY 25 PIPAGEPPPIIGERRSAEPSSARCGGAGAIAMHLLIPRQIYCRNGH-IGTHING 83
 DB 16 ENLPIGNKKPKP-----LYOSMOCHPRLING 44
 QY 94 SVGGTPGPHSHPTTTPISAVAGVISTPVGGLTIOMRKHGKHSSEKLTGCHHGF 113
 DB 45 TVMTKDRSDHMLQIGISAFSVGFVYIKSTPGQYIAMPTSCILVOSQIPSECELEPL 104
 QY 144 FNNWYGVGVYVCHTIGFETVALNRTGTFEZFARFELHCHTHHGFV 175
 DB 105 EHNHYTISR-KHAF-KNMFVIRKNMGSKPCHLTHYSGAILLEPLV 152
 RESULT 45
 FQFL_MOUSE STANDARD: PRT: 155 AA.
 AC P10935;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-INT-1989 (Rel. 11, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HEPARIN-BINDING GROWTH FACTOR 1 PROPEP (HGCF-1) (ACTING FIBROBLAST
 DE GROWTH FACTOR) (AFGF).
 GN FGF1 OR FGF-1 OR PGFA.
 OS Mus musculus (mouse), and
 OS Rattus norvegicus (rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090, 10116;
 RN 11
 RP SEQUENCE FROM N.A.

KC SPECIES Rat;
 KX MEDLINE 89246051; PubMed-2473029;
 EA South et al., Yan C-Y, Balabaud F., Munson P.F.;
 RT "The nucleotide sequence of rat heparin binding growth factor 1
 RT (HGCF-1)".
 RI Nucleic Acids Res. 17:2867-2867 (1989).
 KM 12
 KM SEQUENCE FROM N.A.
 KC SPECIES Mouse;
 KX MEDLINE 9020167; PubMed-2418443;
 RA Robert J.M., Basilico C., Goldfarb M., Hanb O., Martin G.R.;
 RT "Isolation of cDNAs encoding four mouse FGF family members and
 RT characterization of their expression patterns during embryogenesis".
 RI Dev. Biol. 140:451-464 (1990).
 KM 13
 KM SEQUENCE FROM N.A.
 KX MEDLINE 97129432; PubMed-8972905;
 RA Medini F., Harkshaw K.V., Chiu J.M.;
 RT "Cloning and characterization of the mouse Fgf 1 gene".
 RI Gene 179:231-236 (1996).
 KM 14
 KM SEQUENCE FROM N.A.
 KX SPECIES Mouse; ALBAH BALB/C;
 KX MEDLINE 9794746; PubMed-869980;
 RA Adam K.Y., Frostholm A., Harkshaw K.V., Evans J.E., Rother A.,
 RA Chiu J.M.;
 RT "Characterization of the 1b promoter of fibroblast growth factor 1
 RT and its expression in the adult and developing mouse brain".
 RI J. Biol. Chem. 271:30263-30271 (1996).
 CC FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANTI-GENIC AGENTS
 CC IN VIVO AND ARE PARTIAL MITOGENS FOR A VARIETY OF CELL TYPES IN
 CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC -1 SUBUNIT: MONOMER.
 CC -1 SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC
 DR EMBL: X14332; GMA22448.1;
 DR EMBL: M10641; AAA7618.1;
 DR EMBL: U56459; AAC52969.1;
 DR EMBL: U56457; AAC52969.1; JOINED.
 DR EMBL: U56458; AAC52969.1; JOINED.
 DR EMBL: U67610; AAC52907.1;
 DR F1R: S04147; S04147.
 DR F1R: D37460; D37460.
 DR HSSP: P05230; ZAXM.
 DR GDB: M19515; FGF1.
 DR InterPro: IPR002209; HGCF_FGF.
 DR InterPro: IPR002448; ILL_HGCF.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR00262; ILLHGCF.
 DR PRODOM: PD000841; HGCF_FGF_1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HGCF_FGF_1.
 KW Growth factor; Mitogen; Vascularization; Heparin-binding.
 FT PROPEP 1 15
 FT CHAIN 16 155 HEPARIN-BINDING GROWTH FACTOR 1.
 FT BINDING 24 28 HEPARIN (HEPENTANAL).
 FT BINDING 113 116 HEPARIN (HEPENTANAL).
 SQ SEQUENCE 155 AA; 17418 MW; 8880B4F9HAA161 CMC64;
 Query Match 22.8%; Score 254.5; DB 1; Length 155;
 Best local similarity 43.5%; Pred. No. 7; Seq. 17;

RESULT 50
 FGF2_BOVIN
 ID FGF2_BOVIN STANDARD PRT 155 AA
 AC P03969
 DT 23-OCT-1986 (rel. 02, Created)
 DT 23-OCT-1986 (rel. 02, Last sequence update)
 DT 01-FEB-1996 (rel. 33, Last annotation update)
 DE HEPARIN-BINDING GROWTH FACTOR-2 PRECURSOR (HGF-2) (BASIC FIBROBLAST
 DE GROWTH FACTOR) (BFGF) (PROSTATROPIN) [COMPLAINS: KIDNEY-DERIVED GROWTH
 DE FACTOR]
 GN FGF2 OR FGF-2
 OS Bos taurus (Bovine)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Molesteomii;
 OC Mammalia; Eumetazoa; Cetartiodactyla; Fumiviviparia; Bovidae;
 OC Bovidae; Bovinae; Bos
 OX NCBI_Taxid:9913
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Abraham J.A., Merz J.A., Whang J.L., Tumolo A., Friedman J.,
 RA Hjertqvist K.A., Gospodarowicz D., Fiddes J.C.?
 RT "Nucleotide sequence of a bovine clone encoding the angiogenic
 RT protein, basic fibroblast growth factor";
 RT Science 233:545-548(1986)
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE:87217066; PubMed:3472745
 RA Abraham J.A., Whang J.L., Tumolo A., Merz J.A., Fiddes J.C.?
 RT "Human basic fibroblast growth factor: nucleotide sequence, genomic
 RT organization, and expression in mammalian cells";
 RT Cold Spring Harb. Symp. Quant. Biol. 51:657-668(1986)
 RN [3]
 RP SEQUENCE OF 10-155
 RA MEDLINE:86016721; PubMed:3862109
 RA Esch F., Baird A., Ling N., Orre N., Hill F., Gendrey J., Rappaport R.,
 RA Gospodarowicz D., Boehlen P., Gullermin R.?
 RT "Primary structure of bovine pituitary basic fibroblast growth factor
 RT (FGF) and comparison with the amino-terminal sequence of bovine brain
 RT acidic FGF";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:6507-6511(1985)
 RN [4]
 RP SEQUENCE OF 1-9
 RA MEDLINE:86295747; PubMed:3741423
 RA Ueno N., Baird A., Esch F., Ling N., Gullermin R.?
 RT "Isolation of an amino terminal extended form of basic fibroblast
 RT growth factor";
 RT Biochem. Biophys. Res. Commun. 138:590-592(1986)
 RN [5]
 RP SEQUENCE OF 25-41
 RA MEDLINE:8605426; PubMed:4081126
 RA Ueno N., Baird A., Esch F., Shimasaki S., Ling N., Gullermin R.?
 RT "Purification and partial characterization of a mitogenic factor from
 RT bovine liver: structural homology with basic fibroblast growth
 RT factor";
 RT Regul. Pept. 16:135-145(1986)
 RN [7]
 RP X-BAY CRYSTALLOGRAPHY (3.0 ANGSTROMS)
 RA MEDLINE:91095983; PubMed:1702556
 RA Hsu H.T., Kamiya H., Chirino A., Faham S., Fox G.M., Arakawa T.?
 RT "Three-dimensional structures of acidic and basic fibroblast growth
 RT factors";
 RT Science 251:90-93(1991).

CC 1- FUNCTION. THE HEPARIN BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
 CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
 CC VITRO. THERE ARE DIFFERENCES IN THE HEPARIN AFFINITY AND
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC 1- SUBUNIT MONOMER.
 CC 1- MISCELLANEOUS. THIS PROTEIN BINDS HEPARIN MORE TIGHTLY THAN DOES
 CC AFGF.
 CC 1- SIGNIFICANCE. SEE ALSO THE HEPARIN BINDING OF WITH FACT AS FAMILY.
 CC THIS SWISS PROTEIN ENTRY IS COPYRIGHTED. IT IS PRODUCED THROUGH A COLLABORATION
 CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION
 CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
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 CC PURPOSES TO PROVIDE A FREE SERVICE TO THE BIOLOGICAL COMMUNITY.
 CC OR SEND AN EMAIL TO LICENSE@db.psl.fr.
 CC EMBL: M3440; AAA40518.1
 CC PIR: A24654; CEROB.
 CC PIR: A24819; A24819.
 CC PIR: A28278; A28278.
 CC PDH: 1BAG; 31-OCT-93.
 CC InterPro: IPR022099; HGCF_FGF.
 CC InterPro: IPR023489; ILI_HGCF.
 CC Pfam: PF00167; FGF_1.
 CC PRINTS: PR002627; ILIHGF.
 CC PRINTS: PR002635; HGCF_FGF.
 CC PRODOM: P0000843; HGCF_FGF_1.
 CC SMART: SM00442; FGF_1.
 CC PROSITE: PS00247; HGCF_FGF_1.
 CC Growth factor: Mitogenic Vascularization; Hepato-binding;
 CC 3D-structure.
 FT PROPEP 1 9
 FT CHAIN 10 155
 FT SITE 25 155 KIDNEY-DERIVED GROWTH FACTOR.
 FT SITE 46 48 CELL ATTACHMENT SITE (POTENTIAL).
 FT SITE 88 90 CELL ATTACHMENT SITE (POTENTIAL).
 FT BINDING 27 41 HEPARIN (POTENTIAL).
 FT BINDING 116 119 HEPARIN (POTENTIAL).
 FT STRAND 40 44
 FT TURN 35 38
 FT TURN 39 43
 FT TURN 45 46
 FT STRAND 49 52
 FT TURN 55 56
 FT STRAND 58 60
 FT STRAND 62 68
 FT TURN 69 70
 FT STRAND 71 76
 FT TURN 77 80
 FT STRAND 81 85
 FT TURN 87 94
 FT STRAND 91 94
 FT HELIX 95 101
 FT STRAND 103 107
 FT TURN 109 110
 FT STRAND 113 117
 FT TURN 121 122
 FT STRAND 124 124
 FT STRAND 127 127
 FT TURN 129 140
 FT STRAND 133 143
 FT STRAND 136 148
 FT TURN 141 142
 FT HELIX 144 146
 FT STRAND 148 151
 CC SEQUENCE 155 AA, 17250 MW, 3703706.07125 GRAMMAD

Query Match 18.7% Score 2099 108 1 Length 155
 Best Local Similarity 47.5% Pred. No. 1,40 12
 Matches 54: Conservative 209 Mismatches 60: Indels 10: Gaps 4

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2002, 09:53:24 : Search time 23.45 seconds

(without alignments)
1316.139 Million cell updates/sec

Title: US-09-609-543-2

Perfect score: 1118
Sequence: 1 MAPLAEVGRHQAHPKIGQD PPIVPEPVYKRLIMT 211

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14527229 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database :

- 1: SP_archaea:*
- 2: SP_bacteria:*
- 3: SP_fungi:*
- 4: SP_human:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_muc:*
- 8: SP_orfanelle:*
- 9: SP_plant:*
- 10: SP_prodent:*
- 11: SP_virus:*
- 13: SP_vertebrate:*
- 14: SP_unclassified:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1074	96.1	212	11 Q9E8T9	Q9E8T9 rat musc...
2	1069	95.6	212	11 Q9E8T9	Q9E8T9 rat musc...
3	904.5	80.9	208	13 Q9E8T9	Q9E8T9 rat musc...
4	797.5	64.3	207	11 Q9E8T9	Q9E8T9 rat musc...
5	700.5	62.7	207	11 Q9E8T9	Q9E8T9 rat musc...
6	316.5	28.3	253	13 Q9IA15	Q9IA15 galinus g...
7	316	28.3	237	13 Q9IA15	Q9IA15 galinus g...
8	312	27.6	252	11 Q9E8T9	Q9E8T9 rat musc...
9	304.5	27.2	212	13 Q9E8T9	Q9E8T9 rat musc...
10	304	27.2	302	11 Q9E8T9	Q9E8T9 rat musc...
11	303.5	27.1	245	13 Q9E8T9	Q9E8T9 rat musc...
12	303	27.1	199	13 Q9IA15	Q9IA15 galinus g...
13	299	26.4	192	11 Q9E8T9	Q9E8T9 rat musc...
14	295.5	26.4	213	6 Q9E8T9	Q9E8T9 rat musc...
15	294	25.8	243	13 Q9E8T9	Q9E8T9 rat musc...
16	288	25.8	181	13 Q9E8T9	Q9E8T9 rat musc...
17	279	25.0	127	4 Q9E8T9	Q9E8T9 rat musc...
18	279	25.0	191	13 Q9E8T9	Q9E8T9 rat musc...
19	279	24.9	125	5 Q9E8T9	Q9E8T9 rat musc...

20	272.5	24.4	206	12 Q9E8T9	Q9E8T9 rat musc...
21	266	24.8	196	13 Q9E8T9	Q9E8T9 rat musc...
22	262	24.4	185	11 Q9E8T9	Q9E8T9 rat musc...
23	248.5	21.3	129	4 Q9E8T9	Q9E8T9 rat musc...
24	214.5	19.2	196	4 P78442	P78442 homo sapien
25	213	19.1	770	5 P91672	P91672 drosophila
26	213	19.1	770	5 Q9E8T9	Q9E8T9 rat musc...
27	204.5	18.3	106	6 Q9E8T9	Q9E8T9 rat musc...
28	202.5	18.1	130	6 Q9E8T9	Q9E8T9 rat musc...
29	194.5	17.4	125	13 Q9E8T9	Q9E8T9 rat musc...
30	193.5	17.3	97	4 Q9E8T9	Q9E8T9 rat musc...
41	187	15.7	170	11 Q9E8T9	Q9E8T9 rat musc...
42	176.5	15.8	101	13 Q9E8T9	Q9E8T9 rat musc...
43	176.5	15.8	210	13 Q9E8T9	Q9E8T9 rat musc...
44	172	15.4	111	6 Q9E8T9	Q9E8T9 rat musc...
45	171.5	15.3	210	13 Q9E8T9	Q9E8T9 rat musc...
46	170.5	15.2	182	13 Q9E8T9	Q9E8T9 rat musc...
37	169.5	15.2	200	13 Q9E8T9	Q9E8T9 rat musc...
38	169.5	15.2	204	13 Q9E8T9	Q9E8T9 rat musc...
39	168	15.0	74	6 Q9E8T9	Q9E8T9 rat musc...
40	165	14.8	108	6 Q9E8T9	Q9E8T9 rat musc...
41	163.5	14.6	212	13 Q9E8T9	Q9E8T9 rat musc...
42	155	13.9	207	13 Q9E8T9	Q9E8T9 rat musc...
43	153	13.7	73	6 Q9E8T9	Q9E8T9 rat musc...
44	152	13.6	145	13 Q9E8T9	Q9E8T9 rat musc...
45	146.5	13.1	182	12 Q9E8T9	Q9E8T9 rat musc...
46	144	12.9	227	13 Q9E8T9	Q9E8T9 rat musc...
47	141	12.6	78	11 Q9E8T9	Q9E8T9 rat musc...
48	142.5	11.9	87	13 Q9E8T9	Q9E8T9 rat musc...
49	142.5	11.9	87	13 Q9E8T9	Q9E8T9 rat musc...
50	123	11.0	76	6 Q9E8T9	Q9E8T9 rat musc...

ALIGNMENTS

RESULT	1	PRELIMINARY	PRT	212 AA
Q9E8T9	Q9E8T9	Q9E8T9		
AC	Q9E8T9	Q9E8T9		
DT	01-MAR-2001 (TREMUR, 16, created)			
DT	01-MAR-2001 (TREMUR, 16, last sequence update)			
DT	01-JUN-2001 (TREMUR, 17, last annotation update)			
GN	PGF-20.			
OS	Rattus norvegicus (rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid 10116;			
RP	111			
RF	SEQUENCE FROM N.A.			
KC	TISSUE: ADIP. BRAIN;			
KX	PUBMED-11032730;			
KA	Chamchi S., Watanabe Y., Mikami I., Kase N., Ito T., Aizawa A.,			
ET	Feb 02.			
PT	"PGF-20, a novel secreted adipogenic protein, is specifically expressed in the			
KL	substantia nigra pars compacta of rat brain."			
DR	Euk. J. Biochem. 277: 355-360(2000).			
DR	EMBL: A028025; F041376.1; ...			
DR	InterPro: IPR002499; HGSC_PGF.			
DR	InterPro: IPR002499; HGSC_PGF.			
DR	PIR: P00157; F091.1.			
DR	PRINTS: F00362; I1HBGF.			
DR	ProDom: P000831; HGSC_PGF.1.			
DR	SMART: SM00442; F091.1.			
DR	PROSITE: P500247; HGSC_PGF.1.			
SC	SEQUENCE 212 AA, 23677 MW, 495909772077 Q9E8T9			

Query Match: 96.1% Score 1074: 106.1% Length 212:
Post-local similarity: 97.4% Pct ID: 20.93%
Matches: 201, Conserved: 7, Mismatches: 7, Gaps: 0

DR PRODOM: PD000841: HRGF_FGF_1
 DR SMART: SM00442: FGF_1
 DR PROSITE: PS00247: HGF_FGF_1
 SO SEQUENCE 207 AA: 23739 MW: 6280460596266 CHG64

Query Match 64.7% Score 707.5; DB 11; Length 207;
 Host Local Similarity 64.7%; Pred. No. 6.9e-59;
 Matches 144; Conservative 27; Mismatches 40; Indels 11; Gaps 4;

QY 4 LAEVGPTGPTTETGAGGVSSEHLLPAGPPTLGGPAAAFESASLHGMAALV 58
 DQ 1 LAEVGVSASLMDLQGGSSSLGN---VPLADSPHPI NPKIGLPGKIGWSP--TTPA 54
 DB 1 MAEVGVASLMDLQGGSSSLGN---VPLADSPHPI NPKIGLPGKIGWSP--TTPA 54
 QY 59 HILGILRRQIVCTGPGHPIITPSSVCTGPDHSPCTLPPTSAVAVLSIPVDSGLY 118
 DB 55 HIKRIIPRQIVCTGPGHPIITPSSVCTGPDHSPCTLPPTSAVAVLSIPVDSGLY 114
 QY 119 LGMNPRTIYVSKRTIPRPPVPEPPEVPELITLAW 210
 DB 115 LGMNPRTIYVSKRTIPRPPVPEPPEVPELITLAW 210
 QY 179 APSKPGKPTPELPVPVPEVPELITLAW 210
 DB 175 YPRPQKPTPELPVPVPEVPELITLAW 206

RESULT 5

Q9ESL8 Q9ESL8 PRELIMINARY: PROT: 207 AA.
 AC Q9ESL8
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE FIBROBLAST GROWTH FACTOR 16.
 GN FGF16.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Itoh N.
 RT "Mus musculus mRNA for FGF-16 (FGF16)."
 RI Submitted (Seq. Data) to the EMBL/GenBank/DDBJ databases
 RI EMBL: AB049219; BAB16405.1; -
 DR MGC: MGC1041627; Fgf16
 DR InterPro: IPR002209; HRGF_FGF
 DR InterPro: IPR002348; 111_HRGF
 DR Pfam: PF00167; FGF_1
 DR PRINTS: PR00062; FGF16
 DR PRODOM: PD000841; HRGF_FGF_1
 DR SMART: SM00442; FGF_1
 DR PROSITE: PS00247; HGF_FGF_1
 SO SEQUENCE 207 AA: 23751 MW: 6880389041846 CHG64

Query Match 64.7% Score 700.5; DB 11; Length 207;
 Host Local Similarity 64.7%; Pred. No. 4.2e-56;
 Matches 143; Conservative 27; Mismatches 41; Indels 11; Gaps 4;

QY 4 LAEVGPTGPTTETGAGGVSSEHLLPAGPPTLGGPAAAFESASLHGMAALV 58
 DQ 1 LAEVGVSASLMDLQGGSSSLGN---VPLADSPHPI NPKIGLPGKIGWSP--TTPA 54
 DB 1 MAEVGVASLMDLQGGSSSLGN---VPLADSPHPI NPKIGLPGKIGWSP--TTPA 54
 QY 59 HILGILRRQIVCTGPGHPIITPSSVCTGPDHSPCTLPPTSAVAVLSIPVDSGLY 118
 DB 55 HIKRIIPRQIVCTGPGHPIITPSSVCTGPDHSPCTLPPTSAVAVLSIPVDSGLY 114
 QY 119 LGMNPRTIYVSKRTIPRPPVPEPPEVPELITLAW 210
 DB 115 LGMNPRTIYVSKRTIPRPPVPEPPEVPELITLAW 210

QY 179 APSKPGKPTPELPVPVPEVPELITLAW 210
 DQ 175 YPRPQKPTPELPVPVPEVPELITLAW 206

RESULT 6

Q9IAL5 Q9IAL5 PRELIMINARY: PROT: 254 AA.
 AC Q9IAL5
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE FIBROBLAST GROWTH FACTOR HOMOLOGOUS FA-10R 4 ISOFORM 1B.
 GN FGF-4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID:9041;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuhlme 20112825; Tabled 1044718;
 RA Kumar Saenguan 1; Smallwood P.M.; Nathans J.;
 RT "Isotform diversity among fibroblast growth factor homologous factors
 RT is generated by alternative promoter usage and differential
 RT splicing."
 RI J. Biol. Chem. 275:2589-2597(2000).
 DR EMBL: AF199606; AAF010411; -
 DR InterPro: IPR002209; HRGF_FGF
 DR InterPro: IPR002348; 111_HRGF
 DR Pfam: PF00167; FGF_1
 DR PRINTS: PR00252; 111_HRGF
 DR PRODOM: PD000841; HRGF_FGF_1
 DR SMART: SM00442; FGF_1
 DR PROSITE: PS00247; HGF_FGF_1
 SO SEQUENCE 254 AA: 28640 MW: 5457996467405 CHG64

Query Match 68.4% Score 116.5; DB 11; Length 254;
 Host Local Similarity 48.4%; Pred. No. 6e-22;
 Matches 71; Conservative 44; Mismatches 64; Indels 19; Gaps 4;

QY 22 GSHPLTFASTFHLHRSASLDRGAGGAGLHMLHNTSRKATYPRGFHLLP 81
 DQ GSHMGPTGPTTETGAGGVSSEHLLPAGPPTLGGPAAAFESASLHGMAALV 58
 DB GSHMGPTGPTTETGAGGVSSEHLLPAGPPTLGGPAAAFESASLHGMAALV 58
 QY 92 GSGVCTGPDHSPCTLPPTSAVAVLSIPVDSGLY 141
 DQ 92 GSGVCTGPDHSPCTLPPTSAVAVLSIPVDSGLY 141
 DB 92 GSGVCTGPDHSPCTLPPTSAVAVLSIPVDSGLY 141
 QY 119 LGMNPRTIYVSKRTIPRPPVPEPPEVPELITLAW 210
 DQ 115 LGMNPRTIYVSKRTIPRPPVPEPPEVPELITLAW 210
 DB 115 LGMNPRTIYVSKRTIPRPPVPEPPEVPELITLAW 210

QY 220 VPELV 204
 DQ 213 EHSIH 217

RESULT 7

Q9IAL6 Q9IAL6 PRELIMINARY: PROT: 237 AA.
 AC Q9IAL6
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE FIBROBLAST GROWTH FACTOR HOMOLOGOUS FA-10R 4 ISOFORM 1A (FRANKEN).
 GN FGF-4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID:9041;

EN SEQUENCE FROM N.A.
 RP MEDLINE:20112823; PubMed:10644710;
 RA Minor Subunit 1; Smallwood P.M.; Nathans J.;
 RT "Isoform diversity among fibroblast growth factor homologous factors
 RT is controlled by alternative promoter usage and differential
 RT splicing."
 RL J. Biol. Chem. 275:2589-2597(2000).
 DR EMBL:AF199605; AAF4192.1;
 DR InterPro:IPR002209; HMGF_FGF.
 DR InterPro:IPR002448; H1_HMGF.
 DR Pfam:PF00167; FGF_1.
 DR PRINTS:PR00262; H1_HMGF.
 DR PRODOM:PR000841; HMGF_FGF_1.
 DR SMART:SM00442; FGF_1.
 DR PROSITE:PS00247; HMGF_FGF_1.
 FT NON TER
 SQ SEQUENCE: 257 AA; 26816 MW; 3130767465480822 CRC64;

Query Match 28.4%; Score 316; DB 13; Length 237;
 Best Local Similarity 43.5%; Pred. No. 6; to 22;
 Matches 64; Conservative 31; Mismatches 48; Indels 4; Gaps 2;

QY 60 LKGLRRLQYGRGHGHTLPPSSVGLKQHSLLGLEISVAVGLVSGVSGSYL 119
 DB 57 LKGLVTR-LKQKQYVYLQMHQSSLDQKQSSNSTLPLPVGLRVVVLQGVKGYL 114
 QY 120 GNNKGLVGSFKLSLSPKQGFENNYSSNYKQDGRGVVALNKDTPRCA 179
 DB 115 ANNGGYLYPSLFPKFKFSVENYVYSSMLKQSGKAWFLGAKINQVMKGN 174
 QY 180 KSKKDKETHPRLPRVDFE--VPEPLY 204
 DB 175 RVKKTTPAANERKPLVAVMVERSLH 201

RESULT 8
 ID 090906; PRELIMINARY; PRT: 252 AA.

AC 080906;
 DT 01-JUN-1998 (TREMBL) 08; Created)
 DT 01-NOV-1998 (TREMBL) 08; Last sequence update)
 DT 01-JUN-2001 (TREMBL) 17; Last annotation update)
 DE EHF 4B;
 GN EGF4;
 OS Kattus norvegicus (Rat); and
 OS Mus musculus (Mouse);
 OR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OR Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
 OR NCBI_TaxID 10116; 10090;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE BRAIN;
 RX MEDLINE:96267141; PubMed:9602045;
 RA Yamamoto S.; Mikami T.; Ohbayashi N.; Ohta M.; Itoh N.;
 RT "Structure and expression of a novel isoform of mouse FGF homologous
 RT factor (EHF)-4."
 RL Biochem. Biophys. Acta 1198:38-41(1998).
 DR EMBL:AB008908; BAA41544.1;
 DR EMU:AM009007; BAA41544.1;
 DR HSSP:PO3968; HBAR.
 DR M01:109189; F0114.
 DR InterPro:IPR002209; HMGF_FGF.
 DR Pfam:PF00167; FGF_1.
 DR PRODOM:PR000841; HMGF_FGF_1.
 DR SMART:SM00442; FGF_1.
 DR PROSITE:PS00247; HMGF_FGF_1.
 DE PROTEIN: 252 AA; 26164 MW; 281781EFA63AB44 CRC64;
 SQ SEQUENCE: 252 AA; 26164 MW; 281781EFA63AB44 CRC64;

Query Match 27.3%; Score 312; DB 13; Length 252;
 Best Local Similarity 42.9%; Pred. No. 1; to 21;

Matches 63; Conservative 31; Mismatches 49; Indels 4; Gaps 2;

QY 60 LKGLRRLQYGRGHGHTLPPSSVGLKQHSLLGLEISVAVGLVSGVSGSYL 119
 DB 73 LKGLVTR-LKQKQYVYLQMHQSSLDQKQSSNSTLPLPVGLRVVVLQGVKGYL 130
 QY 120 GNNKGLVGSFKLSLSPKQGFENNYSSNYKQDGRGVVALNKDTPRCA 179
 DB 131 ANNGGYLYPSLFPKFKFSVENYVYSSMLKQSGKAWFLGAKINQVMKGN 190
 QY 180 KSKKDKETHPRLPRVDFE--VPEPLY 204
 DB 191 RVKKTTPAANERKPLVAVMVERSLH 217

RESULT 9
 ID 042407; PRELIMINARY; PRT: 212 AA.

AC 042407;
 DT 01-JAN-1998 (TREMBL) 05; Created)
 DT 01-JUN-1998 (TREMBL) 06; Last sequence update)
 DT 01-JUN-2001 (TREMBL) 17; Last annotation update)
 DE F1P0H1AST GROWTH FACTOR 10
 OS Gallus gallus (Chicken);
 OR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OR Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus;
 GN NCBI_TaxID-9031;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE:97330690; PubMed:9187149;
 RA Yoshioke H.; Nakagawa T.; Yamamoto A.; Araga A.; Ohta T.; Ishimaru Y.;
 RA Yoshioke H.; Kuwana T.; Nishio T.; Yamasaki M.; Itoh N.; Noji S.;
 RT "The mesenchymal factor, FGF10, initiates and maintains the outgrowth
 RT of the chick limb bud through interaction with FGF8, an apical
 RT ectodermal factor."
 RL Development 124:2235-2244(1997).
 DR FMBL:DB6333; BAA24945.1;
 DR HSSP:PO3968; HBAR.
 DR InterPro:IPR002209; HMGF_FGF.
 DR Pfam:PF00167; FGF_1.
 DR PRODOM:PR000841; HMGF_FGF_1.
 DR SMART:SM00442; FGF_1.
 DE PROTEIN: 212 AA; 23621 MW; A84C0932972A0D90 CRC64;
 SQ SEQUENCE: 212 AA; 23621 MW; A84C0932972A0D90 CRC64;

Query Match 27.2%; Score 304.5; DB 13; Length 212;
 Best Local Similarity 37.2%; Pred. No. 6; to 21;
 Matches 67; Conservative 35; Mismatches 67; Indels 11; Gaps 4;

QY 21 VSHHRLPPACGERPLLEPPSAEFSAGGVAA-----GLAHGGLIRKQLYGRTP 75
 DB 37 LQDMLSPATNS-----SSSSSSPSSPSSSAEHSYNNHLDGDKKRYVYRK 92
 QY 76 HLOHLPDQSVQGRQDHSLLGLEISVAVGLVSGVSGSYLGNQKGLVGSFKLS 135
 DB 93 FLKLEKNQVSGTKKKNCPSSLLEITSVLGVAVVYSKSNYLAMKKKGVGSFENS 152
 QY 136 EKLFRPQPENNYSSNYKQDGRGVVALNKDTPRCAKSKKDKETHPRLPRV 195
 DB 153 DKLKLNLENNYNYVAVAKMKR KQKGVVALKQKATKQKTPKPRH;ZMHLIDVY 210

RESULT 10
 ID 09GSX5; PRELIMINARY; PRT: 302 AA.

AC 09GSX5;
 DT 01-JUN-2001 (TREMBL) 17; Created)
 DT 01-JUN-2001 (TREMBL) 17; Last sequence update)
 DT 01-JUN-2001 (TREMBL) 17; Last annotation update)
 DE FIBROBLAST GROWTH FACTOR 12 (FRAGMENT);
 GN FGF12;
 OS Mus musculus (Mouse);

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00 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
01 Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus:
02 Mus_Taxid:10090;
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000 Archaeoptera: Aves: Neornithes: Galliformes: Phasianidae: Phasianinae:
001 Gallus:
002 Gallus_Taxid:9031;
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DB 193 ATIAMVTHPR 205

RESULT 21

Q9YH41

PRELIMINARY:

PRT: 196 AA.

Q9YH41

01-MAY-1998 (EMBLrel. 10, Created)

01-MAY-1998 (EMBLrel. 10, Last sequence update)

01-JUN-2001 (EMBLrel. 17, Last annotation update)

PURATIVE FIBROBLAST GROWTH FACTOR-4.

OC Notophthalmus viridescens (Eastern newt) (Triturus cristatus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae;

OC Notophthalmus.

OC NCBI_TaxID=8316;

FN [1]

RP SEQUENCE FROM N.A.

RA Wot Y.

RT Proliferative Newt Fibroblast Growth Factor-4.

RI EMBL: AF295400; AAC98812.1; HBCF_FGF.

DR EMBL: AF295400; AAC98812.1; HBCF_FGF.

DR HSSP: P09038; HBCF.

DR InterPro: IPR001064; Crystal11n.

DR InterPro: IPR002392; HBCF_FGF.

DR InterPro: IPR002348; HBCF_FGF.

DR Pfam: PF0167; FGF_1.

DR PRINTS: PR00262; HBCF_FGF.

DR PRODOM: PD000831; HBCF_FGF.

DR SMART: SM00442; FGF_1.

DR PROSITE: PS00225; CRYSTAL11N_HBCFAMMA. UNKNOWN.

DR PROSITE: PS00247; HBCF_FGF.

DR PROSITE: PS00247; HBCF_FGF.

SV SEQUENCE 196 AA; 2203 MW; AC688CD989CE9A CIRC64;

SV SEQUENCE 196 AA; 2203 MW; AC688CD989CE9A CIRC64;

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SV SEQUENCE 196 AA; 2203 MW; AC688CD989CE9A CIRC64;

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SV SEQUENCE 196 AA; 2203 MW; AC688CD989CE9A CIRC64;

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SV SEQUENCE 196 AA; 2203 MW; AC688CD989CE9A CIRC64;

SV SEQUENCE 196 AA; 2203 MW; AC688CD989CE9A CIRC64;

PI Submitted (Aug 2002) to the Protein Data Bank (PDB) database.

DR EMBL: AF295400; AAC98812.1; HBCF_FGF.

DR InterPro: IPR002392; HBCF_FGF.

DR InterPro: IPR002348; HBCF_FGF.

DR Pfam: PF0167; FGF_1.

DR PRINTS: PR00262; HBCF_FGF.

DR PRODOM: PD000831; HBCF_FGF.

DR SMART: SM00442; FGF_1.

DR PROSITE: PS00225; CRYSTAL11N_HBCFAMMA. UNKNOWN.

DR PROSITE: PS00247; HBCF_FGF.

DR PROSITE: PS00247; HBCF_FGF.

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

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SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

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SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

SV SEQUENCE 185 AA; 2140 MW; 8D8B6449222488 CIRC64;

FT "An anti-hepatomally cytotrophic and post translationally modified form
 RT of a 25kd basic fibroblast growth factor."
 RL Blochem Biophys Res Commun 164:1567-1574(1989)
 RN [3]
 RP PARTIAL SEQUENCE AND MUTAGENESIS
 RA MEDLINE:91322114; PubMed-1713785;
 RX R. J. Ross W. H. Kuo L. L. M. Miller T. J. Smith H. N. Riddle S. L. P.
 RL "Direct evidence for methylation of arginine residues in high
 RT molecular weight forms of basic fibroblast growth factor."
 RL Cell Regul. 2:87-93(1991).
 RN [4]
 RP CHARACTERIZATION.
 RC TISSUE-BRAIN.
 RX MEDLINE: 87284586; PubMed 3375302.
 RA Meseguer J. D. Joseph-Silverstein J. Manolagas R. E. Rich L. B. R.
 RT "Mr 25,000 heparin binding protein from quinea pig brain is a high
 RT molecular weight form of basic fibroblast growth factor."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5778-5782(1987).
 CC -1- FIRST- AND SECOND- METASTATIC ANTIGENS ARE HIGH- MOLECULAR-
 CC FACTOR, IMPLICATED IN A MULTITUDE OF PHYSIOLOGIC AND PATHOLOGIC
 CC PROCESSES, INCLUDING LIMB DEVELOPMENT, ANGIOGENESIS, WOUND
 CC HEALING, AND TUMOR GROWTH. TERTIAL ANTIGEN AND CHROMATINANT FOR
 CC MESENCHYME-DERIVED CELLS. IMPLICATED IN THE DIFFERENTIATION,
 CC PROLIFERATION, AND MAINTENANCE OF CELLS IN THE CENTRAL NERVOUS
 CC SYSTEM AND IN BONE FORMATION. MAY BE AN ONCOGENIC FACTOR THAT ALSO
 CC ACTIVATES TUMOR NEOVASCULARIZATION (BY SIMILARITY).
 CC -1- SHOWN TO FORM A QUATERNARY COMPLEX WITH TWO FGRL AND AT LEAST
 CC ONE HEPARAN SULFATE (BY SIMILARITY).
 CC -1- ALTERNATIVE PROTEIN SPLICING YIELDS TWO ISOFORMS OF 18 KDA AND 17 KDA
 CC (SHOWN HERE). MAY BE PRODUCED BY USE OF ALTERNATIVE TRANSCRIPTION
 CC INITIATION SITES. BOTH FORMS ARE ACTIVE.
 CC -1- 18 KDA: THE N-TERMINAL OF ISOFORM 18 KDA IS BLOCKED (PROBABLY).
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 CC -1- CAUTION: THERE IS A CONCEPTUAL TRANSLATION. MANY TRANSDUCTIONS WERE
 CC INTERPRETED FROM SEQUENCES 72, 92, 93 AND 119 DEMANDS TO EXTEND THE
 CC SIMILARITY TO THE HUMAN SEQUENCE AS WELL AS ON THE BASIS OF
 CC PARTIAL AMINO-ACID SEQUENCING.
 CC EMPH: 175974; AAAS594.1; ALT-PRAME.
 DR HSSP: P09038; 1H1A.
 DR InterPro: IPRO02209; HMGF_FGF.
 DR InterPro: IPRO03448; ILL_HMGF.
 DR Pfam: P000167; FGF_1.
 DR PRINTS: PR00362; ILLHMGF.
 DR PRODOM: PD000831; HMGF_FGF_1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HMGF_FGF_1.
 KW Growth factor; Mitogen; Vascularization; Heparin-binding;
 KW Alternative initiation; Methylation; Phosphorylation;
 KW Developmental protein.
 FT N-TER 1
 FT NON_CONS 15 16
 FT CHAIN 1 173
 FT CHAIN 22 170
 FT INIT_MET 22 22
 FT DOMAIN 11 14
 FT NON_CONS 50 51
 FT SITE 61 63
 FT SITE 103 105
 FT BINDING 52 53
 FT BINDING 105 105
 FT BINDING 143 159
 FT MOD_RES 4 4
 FT MOD_RES 5 5
 FT MOD_RES 8 8
 FT MOD_RES 88 88
 FT MOD_RES 124 124
 FT SPONDINP 170 AA; 18154 MW; P46R0C746EPEEE GRC545
 Query: M1:1 1773 1773 1773 1773 1773
 Post local Similarity 38.78; Prod.No: 5,50-10;
 Matches 46; Conservat: 18; Inq: 6; Gaps: 1

[illegible]


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RN 111
RP SEQUENCE FROM N.A.
RA STRAIN MEM ZEPALAND; TISSUE LUNG;
RB Characteristic: Stripp n. orowski c., pyan k.m.;
RC "Rabbit partial Korean Invertebrate Growth Factor cDNA (pRKGIF cDNA)";
RL Submitted (FEB 1998) to the EMBL/Genbank/DDBJ databases.
DR EMBL: AF049241; AAC25096.1;
DR HSTS: F05240; AAC2;
DR F0101Pro: IP002239; HMGF_FGF;
DR F0101Pro: IP00167; FGF; 1;
DR F0101Pro: IP000831; HMGF_FGF; 1;
DR SMART: SM00442; FGF; 1;
DR PROSITE: PS00247; HMGF_FGF; 1;
PT NON TER 1 74
ET NON TER 1 74
SU SEQUENCE 74 AA: 8441 MW: 7576PUB660079BBA C6664;

```

Query Match 15.0% Score 108; DB 6; Length 74;
 Best Local Similarity 44.9% Prod. No. 1.1e-08;
 Matches 41; Conservative 17; Mismatches 21; Indels 0; Gaps 0.

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QY 83 GSVGCTKOHSHLPGTLEFISVAVGLSKVNSGTLAMNDKGLGSEKLTSECTPEP 142
DB 6 GSKVCTGPKXNNYIMETISVAVGLKGVSEKYLAMNKKGLYAKKLAELINPEEX 65
QY 143 FEENYNY 151
DB 66 ILENNYNY 74

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RESULT 40
QUNIS7
AC QUNIS7 PRELIMINARY; PRT: 108 AA.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DR EMBL: F05240; AAC2;
DR PROSITE: PS00247; HMGF_FGF; 1;
DR SMART: SM00442; FGF; 1;
DR F0101Pro: IP002239; HMGF_FGF; 1;
DR F0101Pro: IP000831; HMGF_FGF; 1;
DR F0101Pro: IP00167; FGF; 1;
DR F0101Pro: IP000831; HMGF_FGF; 1;
DR SMART: SM00442; FGF; 1;
DR PROSITE: PS00247; HMGF_FGF; 1;
PT NON TER 1 108
ET NON TER 1 108
SU SEQUENCE 108 AA: 12399 MW: 6607872442145676 C6664;

```

Query Match 14.8% Score 165; DB 6; Length 108;
 Best Local Similarity 36.8% Prod. No. 4.6e-08;
 Matches 42; Conservative 17; Mismatches 49; Indels 6; Gaps 1;

```

QY 78 GTHHNSVQCTKOHSHLPGTLEFISVAVGLSKVNSGTLAMNDKGLGSEKLTSEK 137
DB 1 KTHHNSVQCTKOHSHLPGTLEFISVAVGLSKVNSGTLAMNDKGLGSEKLTSEK 60

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C7 138 TFEETVTHVCTVYSENIYEDCTSENVVAARSSGKESGAKKNGKERTHHL 191
DB 61 FFEELFNSNNNTYSEFYS-----SMVAKEKTSYVETQRTYKALIFL 108

```

```

RESULT 41
QUNIS1
AC QUNIS1 PRELIMINARY; PRT: 212 AA.
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DR EMBL: F05240; AAC2;
DR F0101Pro: IP002239; HMGF_FGF; 1;
DR F0101Pro: IP000831; HMGF_FGF; 1;
DR F0101Pro: IP00167; FGF; 1;
DR F0101Pro: IP000831; HMGF_FGF; 1;
DR SMART: SM00442; FGF; 1;
DR PROSITE: PS00247; HMGF_FGF; 1;
PT NON TER 1 212
ET NON TER 1 212
SU SEQUENCE 212 AA: 24523 MW: 3497305941210A6A C6664;

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QY 63 IIEPGLYGER-GPHLGLIPGNSVGTPEQNSIPETLEFISVAVGLSKVNSGTL 120
DB 51 IIRYGLYSTRSKVQVGLVSKKINAMAKDSDSHAKLIVETDFPSKVPKIGAFVYVLC 110
QY 121 EINGGLGAG SEKLISELTELGLDMMYGLVNSGTLAMNDKGLGSEKLTSEK 179
DB 111 MNKKGKGLDSKNGKNGKGVSEKLVINNYTALGNKYTE-----GMYAAI IREKTRKNS 164
QY 180 PSREHDKPTHTLIR 193
DB 165 KTRPCHGPEVYEMKP 178

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Query Match 14.8% Score 163.5; DB 13; Length 212;
 Best Local Similarity 30.6% Prod. No. 1.2e-07;
 Matches 41; Conservative 29; Mismatches 55; Indels 9; Gaps 4;

```

QY 63 IIEPGLYGER-GPHLGLIPGNSVGTPEQNSIPETLEFISVAVGLSKVNSGTL 120
DB 51 IIRYGLYSTRSKVQVGLVSKKINAMAKDSDSHAKLIVETDFPSKVPKIGAFVYVLC 110
QY 121 EINGGLGAG SEKLISELTELGLDMMYGLVNSGTLAMNDKGLGSEKLTSEK 179
DB 111 MNKKGKGLDSKNGKNGKGVSEKLVINNYTALGNKYTE-----GMYAAI IREKTRKNS 164
QY 180 PSREHDKPTHTLIR 193
DB 165 KTRPCHGPEVYEMKP 178

```

QY 174 ТРИДАКСКИК 186

[illegible]

KN 11
RP SOURCE: FROM N. A.

Country	Material	Score	146-75	DB 12	Length	1822
United States	Similitude	44.7%	Prod. No. 4,96-06			
Malaysia	433 - Cement Road	23	Misconduct	53	Indels	7
						4
Uy	64 ANOALUETI	1000	YACHTING	1000	1000	112
DB	17	SALE	1000	1000	1000	75
Uy	113	YACHTING	1000	1000	1000	172
DB	76	SALE	1000	1000	1000	130

RESULT	46.	
090100		
ID	090100	PRELIMINARY; PART: 227 AA.
AC	090100	
DT	01 MAR 2001 (TEMPEROL 16, Created)	
DT	01 MAR 2001 (TEMPEROL 16, Last sequence update)	
DT	01 JUN 2001 (TEMPEROL 17, Last annotation update)	
DE	ETHROBLAST GROWTH FACTOR 19,	
GN	FCF 19,	
OS	Gallus gallus (chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neornithae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	
OX	NCBI TaxID 9031;	
KN	[[
RP	SEQUENCE FROM N.A.	
RX	MEBLINK:20564778; PubMed 11110645;	
KA	Lachlan R.K., Asakura K.O., Burney A.L., Schoenwolf G.C.,	
KA	Radney West P.H.;	
RT	Identical location of synovial signals in the hind limb of	
RT	development. ²	
RL	SEQUENCE 290-1965 (1968,1970).	
DE	EMBL: AF415455; AAC59478.1;	
DE	InterPro: IPRO02209; HMG-FCF;	
DE	InterPro: IPRO02448; I.L.HMG.	
DE	InterPro: IPRO167; FGF 1.	
DE	PRINTS: PR00262; I.L.HMG.	
DE	Prodom: P000084; HMG-FCF 1.	
DE	SMART: SM00442; FGF 1.	
DE	PROSITE: PS00247; HMG-FCF; UNKNOWN 1.	
DE	SEQUENCE 227 AA; 24568 MW; 8750764FPD04FHE2 CRC64;	

RESULT	47		
035340			
ID	035340	PRELIMINARY:	PT: 78 AA.
AC	035340:		
DT	01-JAN-1998 (JREF:rel_05, created)		
DT	01-JAN-1998 (JREF:rel_05, last sequence update)		
FT	01-JUN-2001 (JREF:rel_17, last annotation update)		
PH	PHIPOLAST GROWTH FACTOR 12 (PHIPOLAST GROWTH FACTOR RELATED PROTEIN		
DE	PHIPOLAST GROWTH FACTOR 12 (PHIPOLAST GROWTH FACTOR RELATED PROTEIN		

CC Eukaryotes: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Ramadaia; Euteleostei; Rodentia; Sciurotheria; Muridae; Mus
OX NCBI_TaxID:10090;
RN 111
RN SEQUENCE FROM N.A.
RX MENTLINE:97476481; PubMed:924294;
RA Hartung H., Feldman H., Lovec H., Coullet F., Birtmann D.,
RA Goldfarb M.;
R1 "Murine FGF-12 and FGF-13: expression in embryonic nervous system,
R1 connective tissue and heart";
RL Mech. Dev. 64:31-39(1997);
DR EMBL:AF020739; AAH71608.1; -
DR USSP: P09048; IREF;
DR MGI: MGI:109183; Fg112.
DR TIGR:PTO; IPR002209; HGF; FGF;
DR Pfam: PF00167; FGF; 1;
DR PRODOM: P1000431; HGF; FGF; 1;
DR SMART: SM00442; FGF; 1;
FT NON_TER 78 78
SQ SEQUENCE 78 AA: 8646 MW: ALEBIA7E1B8B01A2 CPG94;

Query Match		12.6%	Score 141	DB 11	Length 78
Best Local Similarity		38.9%	Pred. No. 4, 30-05		
Matches	28	Conservative	20	Mismatches	22
				Gaps	27
QY	60	1 H G L I P P R Q Y K P T P E R M G I L P D S A V N V P T P E M Q S L F G L I E P L I S V A V G L Y S I B C V D S G I Y L I	119		
L6	8	E R G I V T R - L P S Q G C T F L O M H D A G I D G I K P E N S O R I L E N L F V A L K V A I G V A K A S V I V	65		
QY	120	G M N D R G E L Y G S E	141		
D6	66	A M N D E G L Y S S D	77		
RESULT	48				
Q9PTV9		PRELIMINARY:	PKT:	87 AA.	
AC	Q9PTV9				
DT	01-MAY-2000	(1PMBLDEL_13; Created)			


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DI 01-MAY-2000 (ITEMBLREL: 13, last sequence update)
DI 01-JUN-2001 (ITEMBLREL: 17, last annotation update)
DE FIBROBLAST GROWTH FACTOR 3 (FRAGMENT).
GN FGF3.
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
OC Acanthopterygii; Acanthopterygii; Perciformes; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziatidae; Oryzias.
OX NCBI_TaxID=8940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN HNT.
RX MEDLINE:20082974; PubMed:10613850;
RA Onitsuka M., Makino S., Yoda K., Wada H., Naruse K., Mitani H.,
RA Shima A., Ozato K., Kimura M., Inoko H.
RT Construction of a linkage map of the Medaka (Oryzias latipes) and
RT mapping of the mutant locus defective in dorsoventral patterning.
RL Genome Res. 9:1277-1287(1999).
DR FMBI: AH030463; BAA85130.1;
DR HSSP: P03968; IBAR.
DR INTERPRO: IPR002586; Pfam: PF00167; FGF_1;
DR PRINTS: PR00262; ILIHGF.
DR PRODOM: PD000841; HRCF_FGF_1.
DR SMART: SM00442; FGF_1.
DR PROSITE: PS00247; HRCF_FGF_1.
FT NON_TER 1
FT NON_TER 87
SU SEQUENCE 87 AA; 985 MW; E58A366F66E16956 CRC64.

Query Match: 21.9%; Score 132.5; EB 13; Length 87;
Best Local Similarity 34.1%; Pval: No. 3.1e-05;
Matches 29; Conservative 14; Mismatches 29; Indels 17; Gaps 1.

DY 122 NEELEYVEPTEETFEETFEETLLAMNVESSM; 160;Shayiba 129
DY 1 NEEGRIVASVNRKRPFRVPRFLLGVNYASVHSTFELPDQACGSKPSPKRWVS 60
DY 169 INKQTPRPAKSKRSHQKPTPLR 193
DY 61 INKGRPRPGRKPRSTDKSLPLR 85

RESULT 49
Q9PTV8 PRELIMINARY PRT 87 AA.
AC Q9PTV8;
DI 01-MAY-2000 (ITEMBLREL: 13, created)
DI 01-MAY-2000 (ITEMBLREL: 13, last sequence update)
DI 01-JUN-2001 (ITEMBLREL: 17, last annotation update)
DE FIBROBLAST GROWTH FACTOR 3 (FRAGMENT).
GN FGF3.
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
OC Acanthopterygii; Acanthopterygii; Perciformes; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziatidae; Oryzias.
OX NCBI_TaxID=8940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN HNT.
RX MEDLINE:20082974; PubMed:10613850;
RA Onitsuka M., Makino S., Yoda K., Wada H., Naruse K., Mitani H.,
RA Shima A., Ozato K., Kimura M., Inoko H.
RT Construction of a linkage map of the Medaka (Oryzias latipes) and
RT mapping of the mutant locus defective in dorsoventral patterning.
RL Genome Res. 9:1277-1287(1999).
DR FMBI: AH030463; BAA85130.1;
DR HSSP: P03968; IBAR.
DR INTERPRO: IPR002586; HRCF_FGF_1.

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DI 1-ECTPRO: IPR003448; ILI_HRCF.
DI P1am: PF00167; FGF_1.
DI PRINTS: PR00262; ILIHGF.
DI PRODOM: PD000841; HRCF_FGF_1.
DI SMART: SM00442; FGF_1.
DI PROSITE: PS00247; HRCF_FGF_1.
DI NON_TER 1
DI NON_TER 87
SU SEQUENCE 87 AA; 1061 MW; E58A366F66E16956 CRC64.

Query Match: 11.9%; Score 142.5; EB 13; Length 87;
Best Local Similarity 44.1%; Pval: No. 4.1e-05;
Matches 29; Conservative 14; Mismatches 29; Indels 17; Gaps 1.

DY 122 NEELEYVEPTEETFEETFEETLLAMNVESSM; 160;Shayiba 129
DY 1 NEEGRIVASVNRKRPFRVPRFLLGVNYASVHSTFELPDQACGSKPSPKRWVS 60
DY 169 INKQTPRPAKSKRSHQKPTPLR 193
DY 61 INKGRPRPGRKPRSTDKSLPLR 85

RESULT 50
Q9NOV2 PRELIMINARY PRT 76 AA.
AC Q9NOV2;
DI 01-OCT-2000 (ITEMBLREL: 15, created)
DI 01-OCT-2000 (ITEMBLREL: 15, last sequence update)
DI 01-JUN-2001 (ITEMBLREL: 17, last annotation update)
DE BASIC FIBROBLAST GROWTH FACTOR (FRAGMENT).
GN FGF2.
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
OC Acanthopterygii; Acanthopterygii; Perciformes; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziatidae; Oryzias.
OX NCBI_TaxID=8940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FETAL PLACENTAL ARTERY;
RA Zhang J., Tsai S.C., Naruse K.R.
RT Growth factor expression in ovine fetal placental artery endothelial
RT cells.
KL Submitted (RAE 2000) to the EMBL/GenBank/DDBJ databases.
DR FMBI: AF250027; AAF65566.1;
DR INTERPRO: IPR002209; HRCF_FGF;
DR P1am: PF00167; FGF_1;
DR PRINTS: PR00262; ILIHGF.
DR PRODOM: PD000841; HRCF_FGF_1.
DR SMART: SM00442; FGF_1.
DR PROSITE: PS00247; HRCF_FGF_1.
DI NON_TER 1
DI NON_TER 76
SU SEQUENCE 76 AA; 879 MW; 709810299454B20 CRC64.

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Query Match: 11.0%; Score 124; EB 6; Length 76;
Best Local Similarity 49.0%; Pval: No. 0.00021;
Matches 25; Conservative 7; Mismatches 19; Indels 9; Gaps 0.

DY 122 NEELEYVEPTEETFEETFEETLLAMNVESSM; 160;Shayiba 129
DY 1 NEEGRIVASVNRKRPFRVPRFLLGVNYASVHSTFELPDQACGSKPSPKRWVS 60

Search completed: April 11, 2002, 09:56:42
Job time: 198 sec

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